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# 5

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<120> SYNTHETIC ENZYMES FOR THE PRODUCTION OF CONIFERYL  
ALCOHOL, CONIFERYLALDEHYDE, FERULIC ACID, VANILLIN AND  
VANILLIC ACID AND THEIR USE

<130> Bayer-9998-CAC

<140> 09/750,986

<141> 2000-12-28

<150> 196 49 655.1 GERMANY

<151> 1996-11-29

<160> 45

<170> PatentIn Ver. 2.1

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Ala	Arg	Asn	Phe	Arg	Pro	Gln	Gly	Thr	Glu	Leu	Thr	Glu	Thr	Ile	Arg	275	280	285
Val	Gly	Gln	Gly	Lys	Ile	Phe	Ala	Glu	Asp	Leu	Asp	Met	Leu	Glu	Gln	290	295	300
Gln	Gln	Arg	Asn	Leu	Leu	Ala	Tyr	Pro	Glu	Arg	Gln	Leu	Leu	Lys	Leu	305	310	315
Asn	Ile	Asp	Ala	Gly	Gly	Val	Gln	Ser	Arg	Arg	Val	Ile	Asp	Arg	Ile	325	330	335
Leu	Ala	Ala	Glu	Gln	Glu	Ala	Ala	Asp	Ala	Ala	Leu	Ile	Ala	Arg	Ser	340	345	350

Ala Ser

<210> 5

<211> 954

<212> DNA

<213> Pseudomonas sp.

<220>

<221> CDS

<222> (1)..(951)

<223> product = "Vanillin-O-Demethylase"/ gene = "vanB"

<400> 5

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Met Ile Glu Val Ile Ile Ser Ala Met Arg Leu Val Ala Gln Asp Ile	
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att agc ctt gag ttt gtc cgg gct gac ggt ggc ttg ctt ccg cct gtc	96
Ile Ser Leu Glu Phe Val Arg Ala Asp Gly Gly Leu Leu Pro Pro Val	
20 25 30	
gag gcc ggc gcc cac gtc gat gtg cat ctt cct ggc ggc ctg att cgg	144
Glu Ala Gly Ala His Val Asp Val His Leu Pro Gly Gly Leu Ile Arg	
35 40 45	
cag tac tcg ctc tgg aat caa cca ggg gcg cag agc cat tac tgc atc	192
Gln Tyr Ser Leu Trp Asn Gln Pro Gly Ala Gln Ser His Tyr Cys Ile	
50 55 60	
ggt gtt ctg aag gac ccg gcg tct cgt ggt ggt tcg aag gcg gtg cac	240
Gly Val Leu Lys Asp Pro Ala Ser Arg Gly Gly Ser Lys Ala Val His	
65 70 75 80	
gag aat ctt cgc gtc ggg atg cgc gtg caa att agc gag ccg agg aac	288
Glu Asn Leu Arg Val Gly Met Arg Val Gln Ile Ser Glu Pro Arg Asn	
85 90 95	
cta ttc cca ttg gaa gag ggg gtg gag cgg agt ctg ctg ttc gcg ggc	336
Leu Phe Pro Leu Glu Glu Gly Val Glu Arg Ser Leu Leu Phe Ala Gly	
100 105 110	
ggg att ggc att acg ccg att ctg tgt atg gct caa gaa tta gca gca	384
Gly Ile Gly Ile Thr Pro Ile Leu Cys Met Ala Gln Glu Leu Ala Ala	
115 120 125	
cgc gag caa gat ttc gag ttg cat tat tgc gcg cgt tcg acc gac cga	432
Arg Glu Gln Asp Phe Glu Leu His Tyr Cys Ala Arg Ser Thr Asp Arg	
130 135 140	
gcg gcg ttc gtt gaa tgg ctt aag gtt tgc gac ttt gct gat cac gta	480
Ala Ala Phe Val Glu Trp Leu Lys Val Cys Asp Phe Ala Asp His Val	
145 150 155 160	
cgt ttc cac ttt gac aat ggc ccg gat cag caa aaa ctg aat gcc gca	528
Arg Phe His Phe Asp Asn Gly Pro Asp Gln Gln Lys Leu Asn Ala Ala	
165 170 175	
gcg ctg cta gcg gcc gag gcc gaa ggt acc cac ctt tat gtc tgt ggg	576
Ala Leu Leu Ala Ala Glu Ala Glu Gly Thr His Leu Tyr Val Cys Gly	
180 185 190	
ccc ggc ggg ttc atg ggg cat gtg ctt gat acc gcg aag gag cag ggc	624
Pro Gly Gly Phe Met Gly His Val Leu Asp Thr Ala Lys Glu Gln Gly	
195 200 205	
tgg gct gac aat cga ctg cat cga gag tat ttc gcc gcg gcg ccg aat	672

Trp	Ala	Asp	Asn	Arg	Leu	His	Arg	Glu	Tyr	Phe	Ala	Ala	Ala	Pro	Asn	
210						215					220					
gtg	agt	gct	gac	gat	ggc	agt	ttc	gag	gtg	cgg	att	cac	agc	acc	gga	720
Val	Ser	Ala	Asp	Asp	Gly	Ser	Phe	Glu	Val	Arg	Ile	His	Ser	Thr	Gly	
225					230					235					240	
caa	gtg	ctt	cag	gtc	ccc	gcg	gat	caa	acg	gtc	tcc	cag	gtg	ctc	gat	768
Gln	Val	Leu	Gln	Val	Pro	Ala	Asp	Gln	Thr	Val	Ser	Gln	Val	Leu	Asp	
			245						250					255		
gcg	gcc	gga	att	atc	gtt	ccc	gtt	tct	tgt	gag	cag	ggc	atc	tgc	ggg	816
Ala	Ala	Gly	Ile	Ile	Val	Pro	Val	Ser	Cys	Glu	Gln	Gly	Ile	Cys	Gly	
			260					265					270			
act	tgc	atc	act	cgg	gtg	gta	gac	gga	gag	cct	gat	cat	cgt	gac	ttc	864
Thr	Cys	Ile	Thr	Arg	Val	Val	Asp	Gly	Glu	Pro	Asp	His	Arg	Asp	Phe	
		275					280					285				
ttc	ctc	acg	gat	gcg	gag	aag	gca	aag	aac	gac	cag	ttc	acc	ccc	tgt	912
Phe	Leu	Thr	Asp	Ala	Glu	Lys	Ala	Lys	Asn	Asp	Gln	Phe	Thr	Pro	Cys	
	290					295				300						
tgc	tcg	cga	gcc	aag	agc	gcc	tgt	ttg	gtc	ttg	gat	ctc	taa			954
Cys	Ser	Arg	Ala	Lys	Ser	Ala	Cys	Leu	Val	Leu	Asp	Leu				
305					310					315						

<210> 6  
 <211> 317  
 <212> PRT  
 <213> Pseudomonas sp.

<400> 6															
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Ile	Ser	Leu	Glu	Phe	Val	Arg	Ala	Asp	Gly	Gly	Leu	Leu	Pro	Pro	Val
			20					25					30		
Glu	Ala	Gly	Ala	His	Val	Asp	Val	His	Leu	Pro	Gly	Gly	Leu	Ile	Arg
		35					40					45			
Gln	Tyr	Ser	Leu	Trp	Asn	Gln	Pro	Gly	Ala	Gln	Ser	His	Tyr	Cys	Ile
	50				55						60				
Gly	Val	Leu	Lys	Asp	Pro	Ala	Ser	Arg	Gly	Gly	Ser	Lys	Ala	Val	His
	65				70					75					80
Glu	Asn	Leu	Arg	Val	Gly	Met	Arg	Val	Gln	Ile	Ser	Glu	Pro	Arg	Asn
				85					90					95	
Leu	Phe	Pro	Leu	Glu	Glu	Gly	Val	Glu	Arg	Ser	Leu	Leu	Phe	Ala	Gly
		100						105					110		
Gly	Ile	Gly	Ile	Thr	Pro	Ile	Leu	Cys	Met	Ala	Gln	Glu	Leu	Ala	Ala
	115						120					125			

Arg Glu Gln Asp Phe Glu Leu His Tyr Cys Ala Arg Ser Thr Asp Arg  
 130 135 140  
 Ala Ala Phe Val Glu Trp Leu Lys Val Cys Asp Phe Ala Asp His Val  
 145 150 155 160  
 Arg Phe His Phe Asp Asn Gly Pro Asp Gln Gln Lys Leu Asn Ala Ala  
 165 170 175  
 Ala Leu Leu Ala Ala Glu Ala Glu Gly Thr His Leu Tyr Val Cys Gly  
 180 185 190  
 Pro Gly Gly Phe Met Gly His Val Leu Asp Thr Ala Lys Glu Gln Gly  
 195 200 205  
 Trp Ala Asp Asn Arg Leu His Arg Glu Tyr Phe Ala Ala Ala Pro Asn  
 210 215 220  
 Val Ser Ala Asp Asp Gly Ser Phe Glu Val Arg Ile His Ser Thr Gly  
 225 230 235 240  
 Gln Val Leu Gln Val Pro Ala Asp Gln Thr Val Ser Gln Val Leu Asp  
 245 250 255  
 Ala Ala Gly Ile Ile Val Pro Val Ser Cys Glu Gln Gly Ile Cys Gly  
 260 265 270  
 Thr Cys Ile Thr Arg Val Val Asp Gly Glu Pro Asp His Arg Asp Phe  
 275 280 285  
 Phe Leu Thr Asp Ala Glu Lys Ala Lys Asn Asp Gln Phe Thr Pro Cys  
 290 295 300  
 Cys Ser Arg Ala Lys Ser Ala Cys Leu Val Leu Asp Leu  
 305 310 315

<210> 7

<211> 1119

<212> DNA

<213> Pseudomonas sp.

<220>

<221> CDS

<222> (1)..(1116)

<223> product = "Formaldehyd-Dehydrogenase"/ gene =  
"fdh"

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cag atc gtc gaa gtg gac gtg gct ccg ccc aag gcc ggt gaa gtc ctg	96
Gln Ile Val Glu Val Asp Val Ala Pro Pro Lys Ala Gly Glu Val Leu	
20 25 30	
gtg cgg gtc gtg gcc acc ggc gtt tgc cac acc gat gcc tac acc ctg	144
Val Arg Val Val Ala Thr Gly Val Cys His Thr Asp Ala Tyr Thr Leu	
35 40 45	
tcc ggc gct gat tcc gag ggc gtt ttc ccc tgc atc ctt ggt cac gaa	192
Ser Gly Ala Asp Ser Glu Gly Val Phe Pro Cys Ile Leu Gly His Glu	
50 55 60	
ggc ggc ggc att gtc gaa gcg gtg ggc gag ggc gtc acc tcg ctg gcg	240
Gly Gly Gly Ile Val Glu Ala Val Gly Glu Gly Val Thr Ser Leu Ala	
65 70 75 80	
gtc ggc gac cac gtg atc ccg ctc tac acg gcc gaa tgc cgt gag tgc	288
Val Gly Asp His Val Ile Pro Leu Tyr Thr Ala Glu Cys Arg Glu Cys	
85 90 95	
aag ttc ttc aag tcc ggc aag acc aac ctg tgc cag aaa gtg cgt gct	336
Lys Phe Phe Lys Ser Gly Lys Thr Asn Leu Cys Gln Lys Val Arg Ala	
100 105 110	
act cag ggc aag ggt ctg atg ccg gac ggc acc tcc cgc ttc agc tac	384
Thr Gln Gly Lys Gly Leu Met Pro Asp Gly Thr Ser Arg Phe Ser Tyr	
115 120 125	
aac ggt cag ccg atc tac cac tac atg ggc tgc tcg acc ttc tcc gag	432
Asn Gly Gln Pro Ile Tyr His Tyr Met Gly Cys Ser Thr Phe Ser Glu	
130 135 140	
tac acc gtg ctg ccg gaa atc tcc ctg gcg aag att ccc aag aat gcg	480
Tyr Thr Val Leu Pro Glu Ile Ser Leu Ala Lys Ile Pro Lys Asn Ala	
145 150 155 160	
ccg ctg gag aaa gtc tgc ctg ctg ggc tgc ggc gtg acc acc ggc att	528
Pro Leu Glu Lys Val Cys Leu Leu Gly Cys Gly Val Thr Thr Gly Ile	
165 170 175	
ggc gcg gtg ctg aac act gcc aag gtg gag gag ggt gct acc gtg gcc	576
Gly Ala Val Leu Asn Thr Ala Lys Val Glu Glu Gly Ala Thr Val Ala	
180 185 190	
atc ttc ggc ctg ggc ggc atc ggc ttg gcg gcg atc atc ggc gcg aag	624
Ile Phe Gly Leu Gly Gly Ile Gly Leu Ala Ala Ile Ile Gly Ala Lys	
195 200 205	
atg gcc aag gcc tcg cgc atc atc gcc atc gac atc aat ccg tcc aag	672
Met Ala Lys Ala Ser Arg Ile Ile Ala Ile Asp Ile Asn Pro Ser Lys	
210 215 220	
ttc gat gtg gct cgc gag ctg ggc gcc act gac ttc gtc aat ccg aac	720
Phe Asp Val Ala Arg Glu Leu Gly Ala Thr Asp Phe Val Asn Pro Asn	
225 230 235 240	
gat cac gcg aag ccg atc cag gat gtc atc gtc gag atg act gat ggc	768

Asp His Ala Lys Pro Ile Gln Asp Val Ile Val Glu Met Thr Asp Gly	
245 250 255	
ggt gtg gac tac agc ttc gag tgc atc ggc aac gtt cga ctc atg cgc	816
Gly Val Asp Tyr Ser Phe Glu Cys Ile Gly Asn Val Arg Leu Met Arg	
260 265 270	
gca gca ctc gag tgc tgc cac aag ggc tgg ggc gaa tcc gtg atc atc	864
Ala Ala Leu Glu Cys Cys His Lys Gly Trp Gly Glu Ser Val Ile Ile	
275 280 285	
ggc gtg gcg ccg gcg ggg gcc gaa atc aac acc cgt ccg ttc cac ctg	912
Gly Val Ala Pro Ala Gly Ala Glu Ile Asn Thr Arg Pro Phe His Leu	
290 295 300	
gtg acc ggt cgc gtc tgg cgg ggt tgc gcg ttc ggt ggc gta aag ggc	960
Val Thr Gly Arg Val Trp Arg Gly Ser Ala Phe Gly Gly Val Lys Gly	
305 310 315 320	
cgc acc gaa ctg ccg agc tac gtg gag aag gca cag cag ggc gag atc	1008
Arg Thr Glu Leu Pro Ser Tyr Val Glu Lys Ala Gln Gln Gly Glu Ile	
325 330 335	
ccg ctg gac acc ttc atc act cac acc atg ggc ctg gac gac atc aac	1056
Pro Leu Asp Thr Phe Ile Thr His Thr Met Gly Leu Asp Asp Ile Asn	
340 345 350	
acg gcc ttc gac ctg atg gac gaa ggg aag agc atc cgc tct gtt gtt	1104
Thr Ala Phe Asp Leu Met Asp Glu Gly Lys Ser Ile Arg Ser Val Val	
355 360 365	
caa ttg agt cgc tag	1119
Gln Leu Ser Arg	
370	

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<211> 372

<212> PRT

<213> Pseudomonas sp.

<400> 8

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Gln Ile Val Glu Val Asp Val Ala Pro Pro Lys Ala Gly Glu Val Leu
20 25 30

Val Arg Val Val Ala Thr Gly Val Cys His Thr Asp Ala Tyr Thr Leu
35 40 45

Ser Gly Ala Asp Ser Glu Gly Val Phe Pro Cys Ile Leu Gly His Glu
50 55 60

Gly Gly Gly Ile Val Glu Ala Val Gly Glu Gly Val Thr Ser Leu Ala
65 70 75 80

Val Gly Asp His	Val Ile Pro Leu Tyr Thr Ala Glu Cys Arg Glu Cys	
	85	90 95
Lys Phe Phe Lys Ser Gly Lys Thr Asn Leu Cys Gln Lys Val Arg Ala		
	100	105 110
Thr Gln Gly Lys Gly Leu Met Pro Asp Gly Thr Ser Arg Phe Ser Tyr		
	115	120 125
Asn Gly Gln Pro Ile Tyr His Tyr Met Gly Cys Ser Thr Phe Ser Glu		
	130	135 140
Tyr Thr Val Leu Pro Glu Ile Ser Leu Ala Lys Ile Pro Lys Asn Ala		
	145	150 155 160
Pro Leu Glu Lys Val Cys Leu Leu Gly Cys Gly Val Thr Thr Gly Ile		
	165	170 175
Gly Ala Val Leu Asn Thr Ala Lys Val Glu Glu Gly Ala Thr Val Ala		
	180	185 190
Ile Phe Gly Leu Gly Gly Ile Gly Leu Ala Ala Ile Ile Gly Ala Lys		
	195	200 205
Met Ala Lys Ala Ser Arg Ile Ile Ala Ile Asp Ile Asn Pro Ser Lys		
	210	215 220
Phe Asp Val Ala Arg Glu Leu Gly Ala Thr Asp Phe Val Asn Pro Asn		
	225	230 235 240
Asp His Ala Lys Pro Ile Gln Asp Val Ile Val Glu Met Thr Asp Gly		
	245	250 255
Gly Val Asp Tyr Ser Phe Glu Cys Ile Gly Asn Val Arg Leu Met Arg		
	260	265 270
Ala Ala Leu Glu Cys Cys His Lys Gly Trp Gly Glu Ser Val Ile Ile		
	275	280 285
Gly Val Ala Pro Ala Gly Ala Glu Ile Asn Thr Arg Pro Phe His Leu		
	290	295 300
Val Thr Gly Arg Val Trp Arg Gly Ser Ala Phe Gly Gly Val Lys Gly		
	305	310 315 320
Arg Thr Glu Leu Pro Ser Tyr Val Glu Lys Ala Gln Gln Gly Glu Ile		
	325	330 335
Pro Leu Asp Thr Phe Ile Thr His Thr Met Gly Leu Asp Asp Ile Asn		
	340	345 350
Thr Ala Phe Asp Leu Met Asp Glu Gly Lys Ser Ile Arg Ser Val Val		
	355	360 365
Gln Leu Ser Arg		
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<210> 9  
 <211> 1638  
 <212> DNA  
 <213> Pseudomonas sp.

<220>  
 <221> CDS  
 <222> (1)..(1635)  
 <223> product = "gamma-Glutamylcystein-Synthetase" /  
 gene = "gcs"

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 gaa tta acc ctg ctt ctt cgg ggt ggt cgg ggc att gag cgt gaa gcc 96  
 Glu Leu Thr Leu Leu Leu Arg Gly Gly Arg Gly Ile Glu Arg Glu Ala  
 20 25 30  
 ttg cgg gtc gat gtt caa ggt gaa ctg gcg ctg acg cct cac ccg gcg 144  
 Leu Arg Val Asp Val Gln Gly Glu Leu Ala Leu Thr Pro His Pro Ala  
 35 40 45  
 gcg ctt ggc tct gcg ttg acc cat ccg aca att act acg gat tac gcc 192  
 Ala Leu Gly Ser Ala Leu Thr His Pro Thr Ile Thr Thr Asp Tyr Ala  
 50 55 60  
 gag gcc ctg ctt gag ttg atc act cgg ccg gca acc gat tgt gcg caa 240  
 Glu Ala Leu Leu Glu Leu Ile Thr Arg Pro Ala Thr Asp Cys Ala Gln  
 65 70 75 80  
 gcc ttg gct gag ctg gag gag ctt cac cgt ttc gtt cat tcg aga ctt 288  
 Ala Leu Ala Glu Leu Glu Glu Leu His Arg Phe Val His Ser Arg Leu  
 85 90 95  
 gag ggg gag tat ctc tgg aat ctg tcc atg cct ggc aga ttg ccg gtt 336  
 Glu Gly Glu Tyr Leu Trp Asn Leu Ser Met Pro Gly Arg Leu Pro Val  
 100 105 110  
 gat gag caa atc ccg att gct tgg tat gga cca tca aat cca ggc atg 384  
 Asp Glu Gln Ile Pro Ile Ala Trp Tyr Gly Pro Ser Asn Pro Gly Met  
 115 120 125  
 ttg cgc cac gtt tat cgc cgt ggc cta gct ctg cgt tat ggc aag cga 432  
 Leu Arg His Val Tyr Arg Arg Gly Leu Ala Leu Arg Tyr Gly Lys Arg  
 130 135 140  
 atg caa tgc atc gca ggg att cac tac aac tac tca ctg ccg cca gag 480  
 Met Gln Cys Ile Ala Ile Ile His Tyr Asn Tyr Ser Leu Pro Pro Glu  
 145 150 155 160  
 ctt ttc gct gtc ctg acc aag gca gag gtc ggg tct ccc aag tta ctg 528

Leu	Phe	Ala	Val	Leu	Thr	Lys	Ala	Glu	Val	Gly	Ser	Pro	Lys	Leu	Leu	
				165					170					175		
gag	cgc	cag	tca	gca	gct	tac	atg	cgc	caa	att	cgc	aac	ctt	cgg	caa	576
Glu	Arg	Gln	Ser	Ala	Ala	Tyr	Met	Arg	Gln	Ile	Arg	Asn	Leu	Arg	Gln	
			180					185					190			
tac	ggt	tgg	ttg	ctg	gcc	tac	ttg	ttc	ggc	gct	tcc	ccc	gcc	atc	tgc	624
Tyr	Gly	Trp	Leu	Leu	Ala	Tyr	Leu	Phe	Gly	Ala	Ser	Pro	Ala	Ile	Cys	
		195					200					205				
aag	agc	ttc	ttg	ggg	ggc	gag	aga	gat	gag	cta	gct	cgc	atg	ggg	ggc	672
Lys	Ser	Phe	Leu	Gly	Gly	Glu	Arg	Asp	Glu	Leu	Ala	Arg	Met	Gly	Gly	
	210					215					220					
gat	acg	ctt	tac	atg	ccc	tat	gca	acc	agc	ttg	cgc	atg	agt	gac	atc	720
Asp	Thr	Leu	Tyr	Met	Pro	Tyr	Ala	Thr	Ser	Leu	Arg	Met	Ser	Asp	Ile	
225					230					235					240	
ggg	tac	cgc	aac	cgt	gcc	atg	gat	gat	cta	tct	ccc	agc	ctg	aat	gat	768
Gly	Tyr	Arg	Asn	Arg	Ala	Met	Asp	Asp	Leu	Ser	Pro	Ser	Leu	Asn	Asp	
			245						250					255		
ctg	ggt	gcc	tat	att	cgc	gat	att	tgc	cgt	gct	ctt	cac	act	ccc	gat	816
Leu	Gly	Ala	Tyr	Ile	Arg	Asp	Ile	Cys	Arg	Ala	Leu	His	Thr	Pro	Asp	
		260					265					270				
gcc	cag	tac	cag	gcg	ctg	ggt	gtg	ttt	gca	cag	ggc	gag	tgg	cgg	cag	864
Ala	Gln	Tyr	Gln	Ala	Leu	Gly	Val	Phe	Ala	Gln	Gly	Glu	Trp	Arg	Gln	
		275				280						285				
tta	aac	gcc	aat	cta	ttg	cag	ttg	gat	agt	gag	tac	tac	gca	ctg	gcg	912
Leu	Asn	Ala	Asn	Leu	Leu	Gln	Leu	Asp	Ser	Glu	Tyr	Tyr	Ala	Leu	Ala	
	290					295					300					
cga	ccg	aag	tca	gcg	ccc	gag	cgg	ggg	gag	cga	aac	ctg	gat	gct	ctc	960
Arg	Pro	Lys	Ser	Ala	Pro	Glu	Arg	Gly	Glu	Arg	Asn	Leu	Asp	Ala	Leu	
305					310					315					320	
gct	agg	cgt	gga	gtc	cag	tat	gtg	gag	ctg	cgc	gca	ctg	gat	ctc	gat	1008
Ala	Arg	Arg	Gly	Val	Gln	Tyr	Val	Glu	Leu	Arg	Ala	Leu	Asp	Leu	Asp	
			325					330					335			
cca	ttc	tcc	ccg	tta	ggc	att	ggc	ctg	acc	tgc	gcc	aag	ttc	ctc	gat	1056
Pro	Phe	Ser	Pro	Leu	Gly	Ile	Gly	Leu	Thr	Cys	Ala	Lys	Phe	Leu	Asp	
			340				345						350			
ggc	ttt	ttg	ctt	ttc	tgc	ttg	ttg	tct	gag	gcg	ccg	gtt	gat	gat	cga	1104
Gly	Phe	Leu	Leu	Phe	Cys	Leu	Leu	Ser	Glu	Ala	Pro	Val	Asp	Asp	Arg	
		355				360						365				
aat	gcc	cag	cgt	tca	aga	ccg	gga	aaa	tct	gag	cct	ggc	cgg	caa	gta	1152
Asn	Ala	Gln	Arg	Ser	Arg	Pro	Gly	Lys	Ser	Glu	Pro	Gly	Arg	Gln	Val	
	370					375					380					

cg	gc	tca	cct	ggc	tta	aag	ctg	cat	cg	aat	ggt	cag	tcc	att	ctc	1200
Arg	Ala	Ser	Pro	Gly	Leu	Lys	Leu	His	Arg	Asn	Gly	Gln	Ser	Ile	Leu	
385					390					395					400	

ctc	aag	gat	tgg	gcg	cag	gaa	gtg	ttg	acg	gag	gtt	cag	gcc	tgt	gtg	1248
Leu	Lys	Asp	Trp	Ala	Gln	Glu	Val	Leu	Thr	Glu	Val	Gln	Ala	Cys	Val	
				405					410					415		

gaa	ttg	ctc	gac	agt	gca	aat	ggg	ggc	tca	tct	cac	gca	ttg	gct	tgg	1296
Glu	Leu	Leu	Asp	Ser	Ala	Asn	Gly	Gly	Ser	Ser	His	Ala	Leu	Ala	Trp	
			420					425					430			

tca	gca	cag	gag	gaa	aag	gtg	ctt	aat	ccg	gat	tgt	gcg	cca	tca	gct	1344
Ser	Ala	Gln	Glu	Glu	Lys	Val	Leu	Asn	Pro	Asp	Cys	Ala	Pro	Ser	Ala	
		435					440					445				

cag	gtg	ctc	gca	gag	ata	cac	aga	cac	ggt	ggg	agc	ttc	acg	gca	ttt	1392
Gln	Val	Leu	Ala	Glu	Ile	His	Arg	His	Gly	Gly	Ser	Phe	Thr	Ala	Phe	
	450					455					460					

ggt	cgc	caa	tta	gct	atc	gac	cat	gca	aaa	cac	ttc	agt	gcc	tcc	tcg	1440
Gly	Arg	Gln	Leu	Ala	Ile	Asp	His	Ala	Lys	His	Phe	Ser	Ala	Ser	Ser	
465					470					475					480	

ctt	gag	gct	ggc	gta	gcc	aaa	gcg	ctt	gac	ctc	cag	gcg	acg	tcg	tct	1488
Leu	Glu	Ala	Gly	Val	Ala	Lys	Ala	Leu	Asp	Leu	Gln	Ala	Thr	Ser	Ser	
			485						490					495		

ctg	cgc	gag	cag	cat	caa	ttg	gag	gcc	aac	gac	cgt	gcg	cca	ttt	tct	1536
Leu	Arg	Glu	Gln	His	Gln	Leu	Glu	Ala	Asn	Asp	Arg	Ala	Pro	Phe	Ser	
			500					505					510			

gac	tac	ctt	cag	caa	ttc	tcc	ctg	gct	ttc	ggt	caa	tcc	gtc	ggc	gcc	1584
Asp	Tyr	Leu	Gln	Gln	Phe	Ser	Leu	Ala	Phe	Gly	Gln	Ser	Val	Gly	Ala	
		515					520					525				

tct	cgt	gcg	ccc	aac	cct	acc	gcg	cac	ctc	atc	gat	ctg	acc	cct	cct	1632
Ser	Arg	Ala	Pro	Asn	Pro	Thr	Ala	His	Leu	Ile	Asp	Leu	Thr	Pro	Pro	
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gtc	taa															1638
Val																
545																

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 <211> 545  
 <212> PRT  
 <213> Pseudomonas sp.

<400> 10																
Met	Pro	Gln	Thr	Leu	Ala	Gly	Arg	Leu	Ser	Leu	Leu	Ser	Gly	Thr	Asp	
1				5					10					15		

Glu	Leu	Thr	Leu	Leu	Leu	Arg	Gly	Gly	Arg	Gly	Ile	Glu	Arg	Glu	Ala	
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20					25					30					
Leu	Arg	Val	Asp	Val	Gln	Gly	Glu	Leu	Ala	Leu	Thr	Pro	His	Pro	Ala
	35						40					45			
Ala	Leu	Gly	Ser	Ala	Leu	Thr	His	Pro	Thr	Ile	Thr	Thr	Asp	Tyr	Ala
	50					55					60				
Glu	Ala	Leu	Leu	Glu	Leu	Ile	Thr	Arg	Pro	Ala	Thr	Asp	Cys	Ala	Gln
	65					70					75				80
Ala	Leu	Ala	Glu	Leu	Glu	Glu	Leu	His	Arg	Phe	Val	His	Ser	Arg	Leu
				85					90					95	
Glu	Gly	Glu	Tyr	Leu	Trp	Asn	Leu	Ser	Met	Pro	Gly	Arg	Leu	Pro	Val
			100					105					110		
Asp	Glu	Gln	Ile	Pro	Ile	Ala	Trp	Tyr	Gly	Pro	Ser	Asn	Pro	Gly	Met
			115					120					125		
Leu	Arg	His	Val	Tyr	Arg	Arg	Gly	Leu	Ala	Leu	Arg	Tyr	Gly	Lys	Arg
	130						135					140			
Met	Gln	Cys	Ile	Ala	Gly	Ile	His	Tyr	Asn	Tyr	Ser	Leu	Pro	Pro	Glu
	145					150					155				160
Leu	Phe	Ala	Val	Leu	Thr	Lys	Ala	Glu	Val	Gly	Ser	Pro	Lys	Leu	Leu
				165					170					175	
Glu	Arg	Gln	Ser	Ala	Ala	Tyr	Met	Arg	Gln	Ile	Arg	Asn	Leu	Arg	Gln
			180					185					190		
Tyr	Gly	Trp	Leu	Leu	Ala	Tyr	Leu	Phe	Gly	Ala	Ser	Pro	Ala	Ile	Cys
		195					200					205			
Lys	Ser	Phe	Leu	Gly	Gly	Glu	Arg	Asp	Glu	Leu	Ala	Arg	Met	Gly	Gly
	210					215					220				
Asp	Thr	Leu	Tyr	Met	Pro	Tyr	Ala	Thr	Ser	Leu	Arg	Met	Ser	Asp	Ile
	225					230					235				240
Gly	Tyr	Arg	Asn	Arg	Ala	Met	Asp	Asp	Leu	Ser	Pro	Ser	Leu	Asn	Asp
				245					250					255	
Leu	Gly	Ala	Tyr	Ile	Arg	Asp	Ile	Cys	Arg	Ala	Leu	His	Thr	Pro	Asp
		260						265					270		
Ala	Gln	Tyr	Gln	Ala	Leu	Gly	Val	Phe	Ala	Gln	Gly	Glu	Trp	Arg	Gln
		275					280					285			
Leu	Asn	Ala	Asn	Leu	Leu	Gln	Leu	Asp	Ser	Glu	Tyr	Tyr	Ala	Leu	Ala
	290					295					300				
Arg	Pro	Lys	Ser	Ala	Pro	Glu	Arg	Gly	Glu	Arg	Asn	Leu	Asp	Ala	Leu
	305					310					315				320

Ala Arg Arg Gly Val Gln Tyr Val Glu Leu Arg Ala Leu Asp Leu Asp  
                             325                            330                            335  
 Pro Phe Ser Pro Leu Gly Ile Gly Leu Thr Cys Ala Lys Phe Leu Asp  
                             340                            345                            350  
 Gly Phe Leu Leu Phe Cys Leu Leu Ser Glu Ala Pro Val Asp Asp Arg  
                             355                            360                            365  
 Asn Ala Gln Arg Ser Arg Pro Gly Lys Ser Glu Pro Gly Arg Gln Val  
                             370                            375                            380  
 Arg Ala Ser Pro Gly Leu Lys Leu His Arg Asn Gly Gln Ser Ile Leu  
 385                            390                            395                            400  
 Leu Lys Asp Trp Ala Gln Glu Val Leu Thr Glu Val Gln Ala Cys Val  
                             405                            410                            415  
 Glu Leu Leu Asp Ser Ala Asn Gly Gly Ser Ser His Ala Leu Ala Trp  
                             420                            425                            430  
 Ser Ala Gln Glu Glu Lys Val Leu Asn Pro Asp Cys Ala Pro Ser Ala  
                             435                            440                            445  
 Gln Val Leu Ala Glu Ile His Arg His Gly Gly Ser Phe Thr Ala Phe  
                             450                            455                            460  
 Gly Arg Gln Leu Ala Ile Asp His Ala Lys His Phe Ser Ala Ser Ser  
 465                            470                            475                            480  
 Leu Glu Ala Gly Val Ala Lys Ala Leu Asp Leu Gln Ala Thr Ser Ser  
                             485                            490                            495  
 Leu Arg Glu Gln His Gln Leu Glu Ala Asn Asp Arg Ala Pro Phe Ser  
                             500                            505                            510  
 Asp Tyr Leu Gln Gln Phe Ser Leu Ala Phe Gly Gln Ser Val Gly Ala  
                             515                            520                            525  
 Ser Arg Ala Pro Asn Pro Thr Ala His Leu Ile Asp Leu Thr Pro Pro  
                             530                            535                            540  
 Val  
 545

<210> 11  
 <211> 354  
 <212> DNA  
 <213> Pseudomonas sp.  
  
 <220>  
 <221> CDS  
 <222> (1)..(351)  
 <223> product = "Cytochrom C UE-Eugenol-Hydroxylase" /

gene = "chyA"

<400> 11

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Met Met Asn Val Asn Tyr Lys Ala Val Gly Ala Ser Leu Leu Leu Ala  
1 5 10 15

ttc atc tct cag gga gct tgg gca gag agc ccc gca gcc tct ggc aat 96  
Phe Ile Ser Gln Gly Ala Trp Ala Glu Ser Pro Ala Ala Ser Gly Asn  
20 25 30

acc cct gac att tat cga aag acc tgc acc tac tgc cat gag cct act 144  
Thr Pro Asp Ile Tyr Arg Lys Thr Cys Thr Tyr Cys His Glu Pro Thr  
35 40 45

gtc aac aat ggc cgg gtc att gcc cga agc ctc ggg ccg act ctg cga 192  
Val Asn Asn Gly Arg Val Ile Ala Arg Ser Leu Gly Pro Thr Leu Arg  
50 55 60

ggg cgc cag atc cct cca cag tac acg gag tac atg gtg cgt cat gga 240  
Gly Arg Gln Ile Pro Pro Gln Tyr Thr Glu Tyr Met Val Arg His Gly  
65 70 75 80

cgc ggg gca atg cct gca ttc tct gaa gca gaa gtg cct ccg gcg gag 288  
Arg Gly Ala Met Pro Ala Phe Ser Glu Ala Glu Val Pro Pro Ala Glu  
85 90 95

ctg aaa gtt ctg ggc gat tgg att cag caa agc agt gct ccc aaa gac 336  
Leu Lys Val Leu Gly Asp Trp Ile Gln Gln Ser Ser Ala Pro Lys Asp  
100 105 110

gct gga gtc gcg cca tga 354  
Ala Gly Val Ala Pro  
115

<210> 12

<211> 117

<212> PRT

<213> Pseudomonas sp.

<400> 12

Met Met Asn Val Asn Tyr Lys Ala Val Gly Ala Ser Leu Leu Leu Ala  
1 5 10 15

Phe Ile Ser Gln Gly Ala Trp Ala Glu Ser Pro Ala Ala Ser Gly Asn  
20 25 30

Thr Pro Asp Ile Tyr Arg Lys Thr Cys Thr Tyr Cys His Glu Pro Thr  
35 40 45

Val Asn Asn Gly Arg Val Ile Ala Arg Ser Leu Gly Pro Thr Leu Arg  
50 55 60

Gly Arg Gln Ile Pro Pro Gln Tyr Thr Glu Tyr Met Val Arg His Gly  
65 70 75 80

Arg Gly Ala Met Pro Ala Phe Ser Glu Ala Glu Val Pro Pro Ala Glu  
85 90 95

Leu Lys Val Leu Gly Asp Trp Ile Gln Gln Ser Ser Ala Pro Lys Asp  
100 105 110

Ala Gly Val Ala Pro  
115

<210> 13  
<211> 687  
<212> DNA  
<213> Pseudomonas sp.

<220>  
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<222> (1) .. (684)  
<223> gene = "ORF5"

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Met Thr Thr Arg Arg Asn Phe Leu Ile Gly Ala Ser Gln Val Gly Ala  
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ttg gtg atg atg tcg ccg aaa ttg gtc ttc cgt acg ccg ctc aag cag 96  
Leu Val Met Met Ser Pro Lys Leu Val Phe Arg Thr Pro Leu Lys Gln  
20 25 30  
aag ccc gtg cgc atc ctg tcg acc ggg ctg gcc ggt gag caa gag ttt 144  
Lys Pro Val Arg Ile Leu Ser Thr Gly Leu Ala Gly Glu Gln Glu Phe  
35 40 45  
cac tcg atg ctt cgc gcg cga ttg acc cat acg ggt cag gtc gac atc 192  
His Ser Met Leu Arg Ala Arg Leu Thr His Thr Gly Gln Val Asp Ile  
50 55 60  
gcg tcg gta ccg ctg gac gca gct att tgg gct tct ccc gct cga ctt 240  
Ala Ser Val Pro Leu Asp Ala Ala Ile Trp Ala Ser Pro Ala Arg Leu  
65 70 75 80  
gcc cag gca atg gat gcg ttg aat ggt acg cgt ctg atc gct ttt gtt 288  
Ala Gln Ala Met Asp Ala Leu Asn Gly Thr Arg Leu Ile Ala Phe Val  
85 90 95  
gag ccc agg aac gaa ttg ata ctg atg caa ttc ttg atg gat cgc ggg 336  
Glu Pro Arg Asn Glu Leu Ile Leu Met Gln Phe Leu Met Asp Arg Gly  
100 105 110  
gct gcg gtg ctt att caa ggt gag cat gcg gtg gac agc aag ggg gtc 384  
Ala Ala Val Leu Ile Gln Gly Glu His Ala Val Asp Ser Lys Gly Val  
115 120 125  
tct cgg cac gac ttt ctg agt acc cca tcc agt gcg gga att gga ggg 432

Ser	Arg	His	Asp	Phe	Leu	Ser	Thr	Pro	Ser	Ser	Ala	Gly	Ile	Gly	Gly	
130						135					140					
gcg	cta	gcc	gac	agc	ctg	gca	aaa	ggg	ggc	tcg	ccg	ttc	tct	att	tcc	480
Ala	Leu	Ala	Asp	Ser	Leu	Ala	Lys	Gly	Gly	Ser	Pro	Phe	Ser	Ile	Ser	
145					150					155					160	
gtc	cga	gcg	ctt	ggc	tcg	gta	act	gct	cag	cca	aga	agt	aat	cag	agt	528
Val	Arg	Ala	Leu	Gly	Ser	Val	Thr	Ala	Gln	Pro	Arg	Ser	Asn	Gln	Ser	
				165					170					175		
gag	gtg	gcc	acc	cac	tgg	acg	acc	gct	ctg	ggg	acc	tat	tat	gcc	gat	576
Glu	Val	Ala	Thr	His	Trp	Thr	Thr	Ala	Leu	Gly	Thr	Tyr	Tyr	Ala	Asp	
			180					185					190			
atc	gca	gtg	ggg	cgc	tgg	gag	ccg	cag	cgc	gaa	gtg	gcc	agc	tat	gga	624
Ile	Ala	Val	Gly	Arg	Trp	Glu	Pro	Gln	Arg	Glu	Val	Ala	Ser	Tyr	Gly	
		195					200					205				
agt	gga	cta	atc	atg	gcg	gaa	cgg	ctt	gat	cgt	gtt	gcc	tca	acc	ttc	672
Ser	Gly	Leu	Ile	Met	Ala	Glu	Arg	Leu	Asp	Arg	Val	Ala	Ser	Thr	Phe	
	210					215					220					
att	gca	gat	ctc	tga												687
Ile	Ala	Asp	Leu													
225																

<210> 14  
 <211> 228  
 <212> PRT  
 <213> Pseudomonas sp.

<400> 14																
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Leu	Val	Met	Met	Ser	Pro	Lys	Leu	Val	Phe	Arg	Thr	Pro	Leu	Lys	Gln	
			20					25					30			
Lys	Pro	Val	Arg	Ile	Leu	Ser	Thr	Gly	Leu	Ala	Gly	Glu	Gln	Glu	Phe	
		35					40					45				
His	Ser	Met	Leu	Arg	Ala	Arg	Leu	Thr	His	Thr	Gly	Gln	Val	Asp	Ile	
	50					55					60					
Ala	Ser	Val	Pro	Leu	Asp	Ala	Ala	Ile	Trp	Ala	Ser	Pro	Ala	Arg	Leu	
	65				70					75					80	
Ala	Gln	Ala	Met	Asp	Ala	Leu	Asn	Gly	Thr	Arg	Leu	Ile	Ala	Phe	Val	
				85					90					95		
Glu	Pro	Arg	Asn	Glu	Leu	Ile	Leu	Met	Gln	Phe	Leu	Met	Asp	Arg	Gly	
			100					105					110			

Ala Ala Val Leu Ile Gln Gly Glu His Ala Val Asp Ser Lys Gly Val  
115 120 125

Ser Arg His Asp Phe Leu Ser Thr Pro Ser Ser Ala Gly Ile Gly Gly  
130 135 140

Ala Leu Ala Asp Ser Leu Ala Lys Gly Gly Ser Pro Phe Ser Ile Ser  
145 150 155 160

Val Arg Ala Leu Gly Ser Val Thr Ala Gln Pro Arg Ser Asn Gln Ser  
165 170 175

Glu Val Ala Thr His Trp Thr Thr Ala Leu Gly Thr Tyr Tyr Ala Asp  
180 185 190

Ile Ala Val Gly Arg Trp Glu Pro Gln Arg Glu Val Ala Ser Tyr Gly  
195 200 205

Ser Gly Leu Ile Met Ala Glu Arg Leu Asp Arg Val Ala Ser Thr Phe  
210 215 220

Ile Ala Asp Leu  
225

<210> 15  
<211> 1554  
<212> DNA  
<213> Pseudomonas sp.

<220>  
<221> CDS  
<222> (1)..(1551)  
<223> product = " Flavoprotein UE-Eugenol-Hydroxylase" /  
gene = "ehyB"

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Met Glu Ser Thr Val Val Leu Pro Glu Gly Val Thr Pro Glu Gln Phe  
1 5 10 15

acc aaa gcc atc agc gag ttc cgt cag gta ttg ggt gag gac agt gtt 96  
Thr Lys Ala Ile Ser Glu Phe Arg Gln Val Leu Gly Glu Asp Ser Val  
20 25 30

ctt gtc act gct gaa cga gtt gtt ccc tat acg aaa ctc ctc att cct 144  
Leu Val Thr Ala Glu Arg Val Val Pro Tyr Thr Lys Leu Leu Ile Pro  
35 40 45

aca cag gat gat gcc cag tac acc ccg gcc ggt gcc ttg act cct tct 192  
Thr Gln Asp Asp Ala Gln Tyr Thr Pro Ala Gly Ala Leu Thr Pro Ser  
50 55 60

tcg gtg gag cag gtc cag aaa gtc atg ggg atc tgc aat aag tac aag 240  
Ser Val Glu Gln Val Gln Lys Val Met Gly Ile Cys Asn Lys Tyr Lys  
65 70 75 80

atc ccg gta tgg cca atc tct acc ggt cgg aac tgg ggg tat ggg tcc	288
Ile Pro Val Trp Pro Ile Ser Thr Gly Arg Asn Trp Gly Tyr Gly Ser	
85 90 95	
gct tcg cct gca act cct ggg cag atg att ctt gac ctt cgc aag atg	336
Ala Ser Pro Ala Thr Pro Gly Gln Met Ile Leu Asp Leu Arg Lys Met	
100 105 110	
aac aag atc att gag atc gat gtt gag ggg tgt act gcc ctg ctc gag	384
Asn Lys Ile Ile Glu Ile Asp Val Glu Gly Cys Thr Ala Leu Leu Glu	
115 120 125	
ccg ggc gtt acc tac cag cag ctt cac gat tac atc aag gag cac aat	432
Pro Gly Val Thr Tyr Gln Gln Leu His Asp Tyr Ile Lys Glu His Asn	
130 135 140	
ctg ccc ttg atg ctg gat gtg ccg act att ggg cct atg gtt ggc ccg	480
Leu Pro Leu Met Leu Asp Val Pro Thr Ile Gly Pro Met Val Gly Pro	
145 150 155 160	
gtg ggt aac acg ctg gat cga ggc gtt ggt tat acg ccg tac ggc gag	528
Val Gly Asn Thr Leu Asp Arg Gly Val Gly Tyr Thr Pro Tyr Gly Glu	
165 170 175	
cac ttc atg atg cag tgt ggt atg gaa gtc gtc atg gcc gat ggc gaa	576
His Phe Met Met Gln Cys Gly Met Glu Val Val Met Ala Asp Gly Glu	
180 185 190	
atc ctc cgt act ggt atg ggc tcg gtg ccc aaa gcc aag act tgg cag	624
Ile Leu Arg Thr Gly Met Gly Ser Val Pro Lys Ala Lys Thr Trp Gln	
195 200 205	
gca ttc aaa tgg ggc tat ggt cca tat ctg gac ggt atc ttt acc cag	672
Ala Phe Lys Trp Gly Tyr Gly Pro Tyr Leu Asp Gly Ile Phe Thr Gln	
210 215 220	
tcc aac ttt ggt gtt gtg aca aag ctc ggg att tgg ttg atg ccc aag	720
Ser Asn Phe Gly Val Val Thr Lys Leu Gly Ile Trp Leu Met Pro Lys	
225 230 235 240	
ccg cca gtg atc aag tcg ttt atg atc cgt tat ccc aat gaa gct gat	768
Pro Pro Val Ile Lys Ser Phe Met Ile Arg Tyr Pro Asn Glu Ala Asp	
245 250 255	
gtg gtt aag gca att gat gct ttt cgc ccg ctg cgt att act cag ctg	816
Val Val Lys Ala Ile Asp Ala Phe Arg Pro Leu Arg Ile Thr Gln Leu	
260 265 270	
att cct aac gtc gtt ttg ttc atg cac ggc atg tac gaa acg gca atc	864
Ile Pro Asn Val Val Leu Phe Met His Gly Met Tyr Glu Thr Ala Ile	
275 280 285	
tgc cgg acg cgt gct gag gtt act tcg gac cca ggt cct att tct gaa	912
Cys Arg Thr Arg Ala Glu Val Thr Ser Asp Pro Gly Pro Ile Ser Glu	
290 295 300	

gcg gac gcc cgc aaa gca ttc aaa gag cta ggc gtt ggc tac tgg aac	960
Ala Asp Ala Arg Lys Ala Phe Lys Glu Leu Gly Val Gly Tyr Trp Asn	
305 310 315 320	
ggt tac ttc gcg ctt tac ggc aca gaa gag cag ata gcc gtc aat gaa	1008
Val Tyr Phe Ala Leu Tyr Gly Thr Glu Glu Gln Ile Ala Val Asn Glu	
325 330 335	
aag atc gtc cgc ggc atc ctc gaa ccg acg ggg ggt gag atc ctc acc	1056
Lys Ile Val Arg Gly Ile Leu Glu Pro Thr Gly Gly Glu Ile Leu Thr	
340 345 350	
gaa gag gag gct gga gat aac att ctt ttc cat cac cat aag cag ctc	1104
Glu Glu Glu Ala Gly Asp Asn Ile Leu Phe His His His Lys Gln Leu	
355 360 365	
atg aac ggc gag atg aca ttg gag gaa atg aat atc tac cag tgg cgc	1152
Met Asn Gly Glu Met Thr Leu Glu Glu Met Asn Ile Tyr Gln Trp Arg	
370 375 380	
gga gca ggt ggc ggt gct tgc tgg ttt gca ccg gtt gct cag gtc aag	1200
Gly Ala Gly Gly Gly Ala Cys Trp Phe Ala Pro Val Ala Gln Val Lys	
385 390 395 400	
ggg cat gag gca gag cag cag gtc aag ctt gct cag aag gtg ctt gca	1248
Gly His Glu Ala Glu Gln Gln Val Lys Leu Ala Gln Lys Val Leu Ala	
405 410 415	
aag cat ggg ttc gat tac acg gcg ggc ttt gcg att ggt tgg cgc gat	1296
Lys His Gly Phe Asp Tyr Thr Ala Gly Phe Ala Ile Gly Trp Arg Asp	
420 425 430	
ctt cac cat gtg atc gat gtg ctg tac gac cgt agc aat gcc gac gag	1344
Leu His His Val Ile Asp Val Leu Tyr Asp Arg Ser Asn Ala Asp Glu	
435 440 445	
aaa aag cgc gct tac gct tgc ttt gat gaa ttg atc gac gtc ttt gcg	1392
Lys Lys Arg Ala Tyr Ala Cys Phe Asp Glu Leu Ile Asp Val Phe Ala	
450 455 460	
gcc gaa ggc ttt gca agt tac agg acc aat att gcc ttt atg gac aaa	1440
Ala Glu Gly Phe Ala Ser Tyr Arg Thr Asn Ile Ala Phe Met Asp Lys	
465 470 475 480	
gtc gcc tct aag ttc ggc gct gag aat aag agg gtc aat cag aag atc	1488
Val Ala Ser Lys Phe Gly Ala Glu Asn Lys Arg Val Asn Gln Lys Ile	
485 490 495	
aag gct gcc ctt gat cca aac ggc atc atc gct ccc ggc aag tcg ggc	1536
Lys Ala Ala Leu Asp Pro Asn Gly Ile Ile Ala Pro Gly Lys Ser Gly	
500 505 510	
att cat ctt ccc aaa taa	1554
Ile His Leu Pro Lys	
515	

<210> 16  
 <211> 517  
 <212> PRT  
 <213> Pseudomonas sp.

<400> 16

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Thr	Lys	Ala	Ile	Ser	Glu	Phe	Arg	Gln	Val	Leu	Gly	Glu	Asp	Ser	Val
			20					25					30		
Leu	Val	Thr	Ala	Glu	Arg	Val	Val	Pro	Tyr	Thr	Lys	Leu	Leu	Ile	Pro
		35					40					45			
Thr	Gln	Asp	Asp	Ala	Gln	Tyr	Thr	Pro	Ala	Gly	Ala	Leu	Thr	Pro	Ser
	50					55					60				
Ser	Val	Glu	Gln	Val	Gln	Lys	Val	Met	Gly	Ile	Cys	Asn	Lys	Tyr	Lys
65					70					75					80
Ile	Pro	Val	Trp	Pro	Ile	Ser	Thr	Gly	Arg	Asn	Trp	Gly	Tyr	Gly	Ser
				85					90					95	
Ala	Ser	Pro	Ala	Thr	Pro	Gly	Gln	Met	Ile	Leu	Asp	Leu	Arg	Lys	Met
			100					105					110		
Asn	Lys	Ile	Ile	Glu	Ile	Asp	Val	Glu	Gly	Cys	Thr	Ala	Leu	Leu	Glu
		115					120					125			
Pro	Gly	Val	Thr	Tyr	Gln	Gln	Leu	His	Asp	Tyr	Ile	Lys	Glu	His	Asn
	130					135					140				
Leu	Pro	Leu	Met	Leu	Asp	Val	Pro	Thr	Ile	Gly	Pro	Met	Val	Gly	Pro
145					150					155					160
Val	Gly	Asn	Thr	Leu	Asp	Arg	Gly	Val	Gly	Tyr	Thr	Pro	Tyr	Gly	Glu
				165					170					175	
His	Phe	Met	Met	Gln	Cys	Gly	Met	Glu	Val	Val	Met	Ala	Asp	Gly	Glu
			180					185					190		
Ile	Leu	Arg	Thr	Gly	Met	Gly	Ser	Val	Pro	Lys	Ala	Lys	Thr	Trp	Gln
		195					200					205			
Ala	Phe	Lys	Trp	Gly	Tyr	Gly	Pro	Tyr	Leu	Asp	Gly	Ile	Phe	Thr	Gln
	210					215					220				
Ser	Asn	Phe	Gly	Val	Val	Thr	Lys	Leu	Gly	Ile	Trp	Leu	Met	Pro	Lys
225					230					235					240
Pro	Pro	Val	Ile	Lys	Ser	Phe	Met	Ile	Arg	Tyr	Pro	Asn	Glu	Ala	Asp
				245					250					255	
Val	Val	Lys	Ala	Ile	Asp	Ala	Phe	Arg	Pro	Leu	Arg	Ile	Thr	Gln	Leu

260	265	270
Ile Pro Asn Val Val Leu Phe Met His Gly Met Tyr Glu Thr Ala Ile 275 280 285		
Cys Arg Thr Arg Ala Glu Val Thr Ser Asp Pro Gly Pro Ile Ser Glu 290 295 300		
Ala Asp Ala Arg Lys Ala Phe Lys Glu Leu Gly Val Gly Tyr Trp Asn 305 310 315 320		
Val Tyr Phe Ala Leu Tyr Gly Thr Glu Glu Gln Ile Ala Val Asn Glu 325 330 335		
Lys Ile Val Arg Gly Ile Leu Glu Pro Thr Gly Gly Glu Ile Leu Thr 340 345 350		
Glu Glu Glu Ala Gly Asp Asn Ile Leu Phe His His His Lys Gln Leu 355 360 365		
Met Asn Gly Glu Met Thr Leu Glu Glu Met Asn Ile Tyr Gln Trp Arg 370 375 380		
Gly Ala Gly Gly Gly Ala Cys Trp Phe Ala Pro Val Ala Gln Val Lys 385 390 395 400		
Gly His Glu Ala Glu Gln Gln Val Lys Leu Ala Gln Lys Val Leu Ala 405 410 415		
Lys His Gly Phe Asp Tyr Thr Ala Gly Phe Ala Ile Gly Trp Arg Asp 420 425 430		
Leu His His Val Ile Asp Val Leu Tyr Asp Arg Ser Asn Ala Asp Glu 435 440 445		
Lys Lys Arg Ala Tyr Ala Cys Phe Asp Glu Leu Ile Asp Val Phe Ala 450 455 460		
Ala Glu Gly Phe Ala Ser Tyr Arg Thr Asn Ile Ala Phe Met Asp Lys 465 470 475 480		
Val Ala Ser Lys Phe Gly Ala Glu Asn Lys Arg Val Asn Gln Lys Ile 485 490 495		
Lys Ala Ala Leu Asp Pro Asn Gly Ile Ile Ala Pro Gly Lys Ser Gly 500 505 510		
Ile His Leu Pro Lys 515		

<210> 17  
 <211> 861  
 <212> DNA  
 <213> Pseudomonas sp.

<220>  
 <221> CDS  
 <222> (1)..(858)  
 <223> gene = "ORF2"

<400> 17

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Met Ile Ala Ile Thr Ala Gly Thr Gly Ser Leu Gly Arg Ala Ile Val	
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gag cga cta ggg gac tgc ggt ctt atc ggt caa gtt cga ttg acg gct	96
Glu Arg Leu Gly Asp Cys Gly Leu Ile Gly Gln Val Arg Leu Thr Ala	
20 25 30	
cgc gat cct aaa agg ctt cgt gcc gct gcc gag gaa ggg ttt cag gtc	144
Arg Asp Pro Lys Arg Leu Arg Ala Ala Ala Glu Glu Gly Phe Gln Val	
35 40 45	
gct aag gcg gat tac gcc gat att ggg agt ctt gac cag gca tta cag	192
Ala Lys Ala Asp Tyr Ala Asp Ile Gly Ser Leu Asp Gln Ala Leu Gln	
50 55 60	
ggg gta gac gta tta ctc ctg att tct ggt act gca ccc aat gaa ata	240
Gly Val Asp Val Leu Leu Leu Ile Ser Gly Thr Ala Pro Asn Glu Ile	
65 70 75 80	
agg atc caa cag cat aag tcg gtc atc gac gcg gca aaa cga aac ggc	288
Arg Ile Gln Gln His Lys Ser Val Ile Asp Ala Ala Lys Arg Asn Gly	
85 90 95	
gtg tcg cgt att gtg tat acc agc ttc ata aat cca agt act cgc agc	336
Val Ser Arg Ile Val Tyr Thr Ser Phe Ile Asn Pro Ser Thr Arg Ser	
100 105 110	
agg tct att tgg gcc tcc att cat cgt gaa act gag act tac ctc agg	384
Arg Ser Ile Trp Ala Ser Ile His Arg Glu Thr Glu Thr Tyr Leu Arg	
115 120 125	
cag tct ggg gtg aag ttt acg att gtc cga aat aat cag tat gcg tct	432
Gln Ser Gly Val Lys Phe Thr Ile Val Arg Asn Asn Gln Tyr Ala Ser	
130 135 140	
aac ctg gat ctg ttg ctg ctg agg gct caa gac agc gga ata ttt gcc	480
Asn Leu Asp Leu Leu Leu Leu Arg Ala Gln Asp Ser Gly Ile Phe Ala	
145 150 155 160	
att ccc ggg gcg aag ggg cgg gtg gcg tac gtc tct cat cgc gac gtt	528
Ile Pro Gly Ala Lys Gly Arg Val Ala Tyr Val Ser His Arg Asp Val	
165 170 175	
gcc gct gcc atc tgt agt gtc ctg acg acc gcc gga cac gat aac agg	576
Ala Ala Ala Ile Cys Ser Val Leu Thr Thr Ala Gly His Asp Asn Arg	
180 185 190	
atc tac cag ctc aca ggc tct gag gct ctc aat ggg ctc gag atc gcg	624
Ile Tyr Gln Leu Thr Gly Ser Glu Ala Leu Asn Gly Leu Glu Ile Ala	
195 200 205	

gag att ctt ggt ggg gtg ctc ggg cgt cca gtg cgc gcg atg gat gcc 672  
Glu Ile Leu Gly Gly Val Leu Gly Arg Pro Val Arg Ala Met Asp Ala  
210 215 220

ttt atg gtt gaa ggc cta cta agc att tat gcc gct tca ggt gct ggg 768  
Phe Met Val Glu Gly Leu Leu Ser Ile Tyr Ala Ala Ser Gly Ala Gly  
245 250 255

gcc gaa tcg atg cga act tac ata cag cgt cta gtt tgg cct tga 861  
Ala Glu Ser Met Arg Thr Tyr Ile Gln Arg Leu Val Trp Pro  
275 280 285

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Arg Asp Pro Lys Arg Leu Arg Ala Ala Ala Glu Glu Gly Phe Gln Val  
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Gly Val Asp Val Leu Leu Leu Ile Ser Gly Thr Ala Pro Asn Glu Ile  
65 70 75 80

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			100					105					110		

Gln Ser Gly Val Lys Phe Thr Ile Val Arg Asn Asn Gln Tyr Ala Ser  
130 135 140

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Asn Leu Asp Leu Leu Leu Leu Arg Ala Gln Asp Ser Gly Ile Phe Ala
145                      150                      155                      160

Ile Pro Gly Ala Lys Gly Arg Val Ala Tyr Val Ser His Arg Asp Val
                      165                      170                      175

Ala Ala Ala Ile Cys Ser Val Leu Thr Thr Ala Gly His Asp Asn Arg
                      180                      185                      190

Ile Tyr Gln Leu Thr Gly Ser Glu Ala Leu Asn Gly Leu Glu Ile Ala
                      195                      200                      205

Glu Ile Leu Gly Gly Val Leu Gly Arg Pro Val Arg Ala Met Asp Ala
                      210                      215                      220

Ser Pro Asp Glu Phe Ala Ala Ser Phe Arg Glu Ala Gly Phe Pro Glu
225                      230                      235                      240

Phe Met Val Glu Gly Leu Leu Ser Ile Tyr Ala Ala Ser Gly Ala Gly
                      245                      250                      255

Glu Tyr Gln Ser Val Ser Pro Asp Val Gly Leu Leu Thr Gly Arg Arg
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Ala Glu Ser Met Arg Thr Tyr Ile Gln Arg Leu Val Trp Pro
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<210> 19

<211> 1011

<212> DNA

<213> Pseudomonas sp.

<220>

<221> CDS

<222> (1)..(1008)

<223> product = "Alcohol-Dehydrogenase" / gene = "adh"

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15

ctc cag cca act cgg ccc cgc ccg cag ttg aat cat ggc gag gtc ctc 96

Leu Gln Pro Thr Arg Pro Arg Pro Gln Leu Asn His Gly Glu Val Leu

20

25

30

atc agg gtc cat gca gcc tcg ctc aac ttt cgc gat ttg atg atc ttg 144

Ile Arg Val His Ala Ala Ser Leu Asn Phe Arg Asp Leu Met Ile Leu

35

40

45

gcc ggt cgc tat ccg ggt caa atg aaa ccc gat gtg atc ccg ctg tcc 192

Ala Gly Arg Tyr Pro Gly Gln Met Lys Pro Asp Val Ile Pro Leu Ser

50

55

60

gat ggt gct ggc gag att gtg gag gtc ggg cct ggc gta tct tcg gag 240

Asp	Gly	Ala	Gly	Glu	Ile	Val	Glu	Val	Gly	Pro	Gly	Val	Ser	Ser	Glu		
65					70					75					80		
gtg	cag	ggt	cag	cgc	gta	gcc	agc	acc	ttt	ttc	cct	aac	tgg	cgg	gcc	288	
Val	Gln	Gly	Gln	Arg	Val	Ala	Ser	Thr	Phe	Phe	Pro	Asn	Trp	Arg	Ala		
				85					90					95			
gga	aag	att	acc	gag	ccg	gct	att	gag	gtg	tcg	ttg	ggc	ttc	ggt	atg	336	
Gly	Lys	Ile	Thr	Glu	Pro	Ala	Ile	Glu	Val	Ser	Leu	Gly	Phe	Gly	Met		
			100					105					110				
gac	ggg	atg	ctc	gcg	gaa	tac	gtt	gct	ctg	ccc	tat	gag	gca	acg	ata	384	
Asp	Gly	Met	Leu	Ala	Glu	Tyr	Val	Ala	Leu	Pro	Tyr	Glu	Ala	Thr	Ile		
		115					120					125					
ccg	ata	ccg	gag	cac	ctg	tcg	tac	gag	gag	gct	gca	aca	ttg	cct	tgc	432	
Pro	Ile	Pro	Glu	His	Leu	Ser	Tyr	Glu	Glu	Ala	Ala	Thr	Leu	Pro	Cys		
	130					135					140						
gcg	gcg	cta	acc	gct	tggt	aat	gcg	ttg	acc	gaa	gtg	ggg	cgt	gtc	aag	480	
Ala	Ala	Leu	Thr	Ala	Trp	Asn	Ala	Leu	Thr	Glu	Val	Gly	Arg	Val	Lys		
145					150					155					160		
gcc	ggt	gat	acg	gtc	ttg	ttg	ctt	ggc	act	ggc	ggt	gtc	tcg	atg	ttc	528	
Ala	Gly	Asp	Thr	Val	Leu	Leu	Leu	Gly	Thr	Gly	Gly	Val	Ser	Met	Phe		
			165					170						175			
gcg	ttg	cag	ttc	gcc	aag	ctc	ttg	ggg	gcg	acg	gtc	att	cac	acc	tcg	576	
Ala	Leu	Gln	Phe	Ala	Lys	Leu	Leu	Gly	Ala	Thr	Val	Ile	His	Thr	Ser		
			180					185					190				
agc	agt	gaa	caa	aag	ctg	gag	agg	gtg	aaa	gcg	atg	ggg	gct	gat	cat	624	
Ser	Ser	Glu	Gln	Lys	Leu	Glu	Arg	Val	Lys	Ala	Met	Gly	Ala	Asp	His		
		195					200					205					
ctg	atc	aac	tac	cgc	aat	tcg	cca	ggg	tggt	gac	cgt	act	gtc	ctg	gat	672	
Leu	Ile	Asn	Tyr	Arg	Asn	Ser	Pro	Gly	Trp	Asp	Arg	Thr	Val	Leu	Asp		
	210					215					220						
ctc	acc	gcg	ggg	cga	ggg	gtt	gac	ctg	gta	gtc	gag	gta	ggg	ggg	gcg	720	
Leu	Thr	Ala	Gly	Arg	Gly	Val	Asp	Leu	Val	Val	Glu	Val	Gly	Gly	Ala		
225					230					235					240		
ggg	acc	ttg	gag	cgc	tca	ctt	cgt	gcg	gtc	aag	gta	ggc	ggt	att	gtc	768	
Gly	Thr	Leu	Glu	Arg	Ser	Leu	Arg	Ala	Val	Lys	Val	Gly	Gly	Ile	Val		
				245					250					255			
gcc	acg	att	ggg	cta	gtg	gct	ggc	gtt	ggc	ccg	att	gac	cca	ttg	ccg	816	
Ala	Thr	Ile	Gly	Leu	Val	Ala	Gly	Val	Gly	Pro	Ile	Asp	Pro	Leu	Pro		
			260					265					270				
ctt	atc	tcc	agg	gct	att	cag	ctc	tcg	ggc	gtc	tat	gtc	ggt	tcc	cgg	864	
Leu	Ile	Ser	Arg	Ala	Ile	Gln	Leu	Ser	Gly	Val	Tyr	Val	Gly	Ser	Arg		
		275					280					285					
gaa	atg	ttt	ctc	tca	atg	aac	aaa	gcc	att	gca	tca	gcc	gaa	atc	aag	912	
Glu	Met	Phe	Leu	Ser	Met	Asn	Lys	Ala	Ile	Ala	Ser	Ala	Glu	Ile	Lys		

290	295	300	
cca gtg atc gat tgc tgc ttc ccc atc gac gag gtt gga gat gct tat			960
Pro Val Ile Asp Cys Cys Phe Pro Ile Asp Glu Val Gly Asp Ala Tyr			
305	310	315	320
gag tac atg cgt agc ggc aat cac ctt ggc aaa gta gtt atc acg atc			1008
Glu Tyr Met Arg Ser Gly Asn His Leu Gly Lys Val Val Ile Thr Ile			
	325	330	335
taa			1011

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 <212> PRT  
 <213> Pseudomonas sp.

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			20					25					30		
Ile	Arg	Val	His	Ala	Ala	Ser	Leu	Asn	Phe	Arg	Asp	Leu	Met	Ile	Leu
		35					40					45			
Ala	Gly	Arg	Tyr	Pro	Gly	Gln	Met	Lys	Pro	Asp	Val	Ile	Pro	Leu	Ser
	50					55					60				
Asp	Gly	Ala	Gly	Glu	Ile	Val	Glu	Val	Gly	Pro	Gly	Val	Ser	Ser	Glu
65					70					75					80
Val	Gln	Gly	Gln	Arg	Val	Ala	Ser	Thr	Phe	Phe	Pro	Asn	Trp	Arg	Ala
				85					90					95	
Gly	Lys	Ile	Thr	Glu	Pro	Ala	Ile	Glu	Val	Ser	Leu	Gly	Phe	Gly	Met
			100					105					110		
Asp	Gly	Met	Leu	Ala	Glu	Tyr	Val	Ala	Leu	Pro	Tyr	Glu	Ala	Thr	Ile
		115					120					125			
Pro	Ile	Pro	Glu	His	Leu	Ser	Tyr	Glu	Glu	Ala	Ala	Thr	Leu	Pro	Cys
	130					135						140			
Ala	Ala	Leu	Thr	Ala	Trp	Asn	Ala	Leu	Thr	Glu	Val	Gly	Arg	Val	Lys
145					150					155					160
Ala	Gly	Asp	Thr	Val	Leu	Leu	Leu	Gly	Thr	Gly	Gly	Val	Ser	Met	Phe
				165					170					175	
Ala	Leu	Gln	Phe	Ala	Lys	Leu	Leu	Gly	Ala	Thr	Val	Ile	His	Thr	Ser
			180					185					190		
Ser	Ser	Glu	Gln	Lys	Leu	Glu	Arg	Val	Lys	Ala	Met	Gly	Ala	Asp	His
		195					200					205			

Leu Ile Asn Tyr Arg Asn Ser Pro Gly Trp Asp Arg Thr Val Leu Asp  
210 215 220

Leu Thr Ala Gly Arg Gly Val Asp Leu Val Val Glu Val Gly Gly Ala  
225 230 235 240

Gly Thr Leu Glu Arg Ser Leu Arg Ala Val Lys Val Gly Gly Ile Val  
245 250 255

Ala Thr Ile Gly Leu Val Ala Gly Val Gly Pro Ile Asp Pro Leu Pro  
260 265 270

Leu Ile Ser Arg Ala Ile Gln Leu Ser Gly Val Tyr Val Gly Ser Arg  
275 280 285

Glu Met Phe Leu Ser Met Asn Lys Ala Ile Ala Ser Ala Glu Ile Lys  
290 295 300

Pro Val Ile Asp Cys Cys Phe Pro Ile Asp Glu Val Gly Asp Ala Tyr  
305 310 315 320

Glu Tyr Met Arg Ser Gly Asn His Leu Gly Lys Val Val Ile Thr Ile  
325 330 335

<210> 21

<211> 1518

<212> DNA

<213> Pseudomonas sp.

<400> 21

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ccttagccgg aatggcagct tgatgggtgc cacgggacca gactggatgt cttgagtgtc 180  
gagaattacc agatcgctgc gattttcatc gaggcgacca accacggtca gcaagtaccc 240  
gtcaccttcg gcggcggtcg gacttctagg gacgaaggcc ggctcctggg ccgccgagggc 300  
ttcgccggag taccagaggt cgtagtcacc tcggtggttg tcccagatgc cgagtgaatt 360  
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aaagaaatcg ttagccggg ttcgcttgat ctgcgtcgtg ctgctatcga ggtcaatttc 540  
ccaacgagtc aggcgtggta cggctttctc aggggcgaag gggttggtttt gtgagttggg 600  
gaaggggaac ggcaggattt cactttccat aaggtcgata taaatcttgg ttccgacttc 660

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tggtgttttc gccttgaggc gggacaggct gttggtggcc ggcataattg ggaaaatgga 840
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ttcatgtgtc accttgccgt gcttgctgac aatgtaatag gccatgtctg gagttgcttc 960
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tgtacgagga tccagttcgt acggtaggcc gtcttccttc accgccagca ccttgccgtg 1140
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tggcgtatta cggtagaacg ttccatttat tgattttggg atttcgccgt caacctctag 1440
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1518

<210> 22

<211> 505

<212> PRT

<213> Pseudomonas sp.

<400> 22

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Pro Thr Arg Ile Glu Ala Asp Leu Phe Asp Leu Glu Val Asp Gly Glu
          20             25             30

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Ile Pro Lys Ser Ile Asn Gly Thr Phe Tyr Arg Asn Thr Pro Glu Pro
      35             40             45

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Gln Val Thr Pro Gln Lys Phe His Thr Phe Ile Asp Gly Asp Gly Met
  50             55             60

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Ala Ser Ala Phe His Phe Glu Asp Gly His Val Asp Phe Ile Ser Arg
  65             70             75             80

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Trp Val Lys Thr Ala Arg Phe Thr Ala Glu Arg Leu Ala Arg Lys Ser
          85             90             95

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Leu Phe Gly Met Tyr Arg Asn Pro Tyr Thr Asp Asp Thr Ser Val Lys
      100             105             110

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Gly	Leu	Asp	Arg	Thr	Val	Ala	Asn	Thr	Ser	Ile	Ile	Ser	His	His	Gly	
	115						120					125				
Lys	Val	Leu	Ala	Val	Lys	Glu	Asp	Gly	Leu	Pro	Tyr	Glu	Leu	Asp	Pro	
	130					135					140					
Arg	Thr	Leu	Glu	Thr	Arg	Gly	His	Phe	Asp	Tyr	Asp	Gly	Gln	Val	Thr	
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Ser	Gln	Thr	His	Thr	Ala	His	Pro	Lys	Tyr	Asp	Pro	Glu	Thr	Gly	Asp	
				165					170					175		
Leu	Leu	Phe	Phe	Gly	Ser	Ala	Ala	Lys	Gly	Glu	Ala	Thr	Pro	Asp	Met	
			180					185					190			
Ala	Tyr	Tyr	Ile	Val	Asp	Lys	His	Gly	Lys	Val	Thr	His	Glu	Thr	Trp	
	195						200					205				
Phe	Glu	Gln	Pro	Tyr	Gly	Ala	Phe	Met	His	Asp	Phe	Ala	Ile	Thr	Arg	
	210					215					220					
Asn	Trp	Ser	Ile	Phe	Pro	Ile	Met	Pro	Ala	Thr	Asn	Ser	Leu	Ser	Arg	
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Tyr	Ile	Gly	Val	Leu	Ala	Pro	Arg	Gln	Gly	Ser	Leu	Ile	Arg	Trp	Leu	
		260						265					270			
Lys	Ala	Pro	Ala	Leu	Trp	Val	Phe	His	Val	Val	Asn	Ala	Trp	Glu	Val	
	275						280					285				
Gly	Thr	Lys	Ile	Tyr	Ile	Asp	Leu	Met	Glu	Ser	Glu	Ile	Leu	Pro	Phe	
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Pro	Phe	Pro	Asn	Ser	Gln	Asn	Gln	Pro	Phe	Ala	Pro	Glu	Lys	Ala	Val	
305					310					315					320	
Pro	Arg	Leu	Thr	Arg	Trp	Glu	Ile	Asp	Leu	Asp	Ser	Ser	Ser	Asp	Glu	
				325					330					335		
Ile	Lys	Arg	Thr	Arg	Leu	His	Asp	Phe	Phe	Ala	Glu	Met	Pro	Ile	Met	
			340					345					350			
Asp	Ser	Ser	Phe	Ala	Leu	Gln	Cys	Asn	Arg	Tyr	Gly	Phe	Met	Gly	Val	
	355						360					365				
Asp	Asp	Pro	Arg	Lys	Pro	Leu	Ala	His	Gln	Gln	Ala	Glu	Lys	Ile	Phe	
	370					375					380					
Ala	Tyr	Asn	Ser	Leu	Gly	Ile	Trp	Asp	Asn	His	Arg	Gly	Asp	Tyr	Asp	
385					390					395					400	
Leu	Trp	Tyr	Ser	Gly	Glu	Ala	Ser	Ala	Ala	Gln	Glu	Pro	Ala	Phe	Val	
				405					410					415		

Pro Arg Ser Pro Thr Ala Ala Glu Gly Asp Gly Tyr Leu Leu Thr Val  
                   420                  425                  430  
 Val Gly Arg Leu Asp Glu Asn Arg Ser Asp Leu Val Ile Leu Asp Thr  
                   435                  440                  445  
 Gln Asp Ile Gln Ser Gly Pro Val Ala Thr Ile Lys Leu Pro Phe Arg  
                   450                  455                  460  
 Leu Arg Ala Ala Leu His Gly Cys Trp Val Pro Asp Leu Asn Glu Thr  
                   465                  470                  475                  480  
 Pro Thr Phe Gln Pro Phe Arg Ala Pro Val Arg Gly Arg Cys Pro Arg  
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 Thr Asn Phe Gln Ser Arg Ser Arg Arg  
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<210> 23  
 <211> 951  
 <212> DNA  
 <213> Pseudomonas sp.

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 <221> CDS  
 <222> (1)..(948)  
 <223> gene = "ORF3"

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 act ctc gcg gat tcg ccg ctg cat tgg gcg cat acc ctg aat gga tca 96  
 Thr Leu Ala Asp Ser Pro Leu His Trp Ala His Thr Leu Asn Gly Ser  
                   20                  25                  30  
 atg cgt act cat ttc gaa gtc cag cgt ctt gag cgg ggt aga ggt gcc 144  
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                   35                  40                  45  
 tcc ctt gcc cga tct aga ttt ggc gcg ggt gag ctg tac agt gcc att 192  
 Ser Leu Ala Arg Ser Arg Phe Gly Ala Gly Glu Leu Tyr Ser Ala Ile  
                   50                  55                  60  
 gca cca agc cag gta ctt cgc cac ttc aac gac cag cga aat gct gat 240  
 Ala Pro Ser Gln Val Leu Arg His Phe Asn Asp Gln Arg Asn Ala Asp  
                   65                  70                  75                  80  
 gag gct gag cac agc tat ttg att cag ata cga agt ggc gct ttg ggc 288  
 Glu Ala Glu His Ser Tyr Leu Ile Gln Ile Arg Ser Gly Ala Leu Gly  
                   85                  90                  95  
 gtt gca tcc ggc gga aga aag gtg atc ttg gca aat ggt gat tgc tcc 336  
 Val Ala Ser Gly Gly Arg Lys Val Ile Leu Ala Asn Gly Asp Cys Ser

100	105	110	
ata gtt gat agt cgc caa gac ttc aca ctt tcc tcg aac tct tcg acc			384
Ile Val Asp Ser Arg Gln Asp Phe Thr Leu Ser Ser Asn Ser Ser Thr			
115	120	125	
caa ggt gtc gta ata cgc ttt ccg gtg agt tgg ctg gga gcg tgg gtg			432
Gln Gly Val Val Ile Arg Phe Pro Val Ser Trp Leu Gly Ala Trp Val			
130	135	140	
tcc aat ccg gag gat ctt atc gcc cga cga gtt gat gct gag gta ggg			480
Ser Asn Pro Glu Asp Leu Ile Ala Arg Arg Val Asp Ala Glu Val Gly			
145	150	155	160
tgg ggt agg gcg cta agc gca tcg gtt tct aat cta gat cca ttg cgc			528
Trp Gly Arg Ala Leu Ser Ala Ser Val Ser Asn Leu Asp Pro Leu Arg			
165	170	175	
atc gac gat tta ggt agc aat gta aat ggc att gca gag cat gtt gct			576
Ile Asp Asp Leu Gly Ser Asn Val Asn Gly Ile Ala Glu His Val Ala			
180	185	190	
atg tta att tca cta gca agt tct gcg gtt agt tct gaa gat ggg ggt			624
Met Leu Ile Ser Leu Ala Ser Ser Ala Val Ser Ser Glu Asp Gly Gly			
195	200	205	
gtg gct ctt cgg aaa atg agg gaa gtg aag aga gta ctc gag cag agt			672
Val Ala Leu Arg Lys Met Arg Glu Val Lys Arg Val Leu Glu Gln Ser			
210	215	220	
ttc gca gac gct aat ctc ggg ccg gaa agt gtt tca agt caa tta gga			720
Phe Ala Asp Ala Asn Leu Gly Pro Glu Ser Val Ser Ser Gln Leu Gly			
225	230	235	240
att tcg aaa cgc tat ttg cat tat gtc ttt gct gcg tgc ggt acg acc			768
Ile Ser Lys Arg Tyr Leu His Tyr Val Phe Ala Ala Cys Gly Thr Thr			
245	250	255	
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Phe Gly Arg Glu Leu Leu Glu Ile Arg Leu Gly Lys Ala Tyr Arg Met			
260	265	270	
ctc tgt gcg gcg agt gac tcg ggt gct gtg ctg aag gtg gcc atg tcc			864
Leu Cys Ala Ala Ser Asp Ser Gly Ala Val Leu Lys Val Ala Met Ser			
275	280	285	
tca ggt ttt tcg gat tca agc cat ttc agc aag aaa ttt aag gaa aga			912
Ser Gly Phe Ser Asp Ser Ser His Phe Ser Lys Lys Phe Lys Glu Arg			
290	295	300	
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Tyr Gly Val Ser Pro Val Ser Leu Val Arg Gln Ala			
305	310	315	

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<212> PRT  
<213> Pseudomonas sp.

<400> 24

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			20					25					30		
Met	Arg	Thr	His	Phe	Glu	Val	Gln	Arg	Leu	Glu	Arg	Gly	Arg	Gly	Ala
		35					40					45			
Ser	Leu	Ala	Arg	Ser	Arg	Phe	Gly	Ala	Gly	Glu	Leu	Tyr	Ser	Ala	Ile
	50					55					60				
Ala	Pro	Ser	Gln	Val	Leu	Arg	His	Phe	Asn	Asp	Gln	Arg	Asn	Ala	Asp
65					70					75					80
Glu	Ala	Glu	His	Ser	Tyr	Leu	Ile	Gln	Ile	Arg	Ser	Gly	Ala	Leu	Gly
			85						90					95	
Val	Ala	Ser	Gly	Gly	Arg	Lys	Val	Ile	Leu	Ala	Asn	Gly	Asp	Cys	Ser
			100					105					110		
Ile	Val	Asp	Ser	Arg	Gln	Asp	Phe	Thr	Leu	Ser	Ser	Asn	Ser	Ser	Thr
		115					120					125			
Gln	Gly	Val	Val	Ile	Arg	Phe	Pro	Val	Ser	Trp	Leu	Gly	Ala	Trp	Val
	130					135					140				
Ser	Asn	Pro	Glu	Asp	Leu	Ile	Ala	Arg	Arg	Val	Asp	Ala	Glu	Val	Gly
145					150					155					160
Trp	Gly	Arg	Ala	Leu	Ser	Ala	Ser	Val	Ser	Asn	Leu	Asp	Pro	Leu	Arg
				165					170					175	
Ile	Asp	Asp	Leu	Gly	Ser	Asn	Val	Asn	Gly	Ile	Ala	Glu	His	Val	Ala
			180					185					190		
Met	Leu	Ile	Ser	Leu	Ala	Ser	Ser	Ala	Val	Ser	Ser	Glu	Asp	Gly	Gly
		195					200					205			
Val	Ala	Leu	Arg	Lys	Met	Arg	Glu	Val	Lys	Arg	Val	Leu	Glu	Gln	Ser
	210					215					220				
Phe	Ala	Asp	Ala	Asn	Leu	Gly	Pro	Glu	Ser	Val	Ser	Ser	Gln	Leu	Gly
225					230					235					240
Ile	Ser	Lys	Arg	Tyr	Leu	His	Tyr	Val	Phe	Ala	Ala	Cys	Gly	Thr	Thr
				245					250					255	
Phe	Gly	Arg	Glu	Leu	Leu	Glu	Ile	Arg	Leu	Gly	Lys	Ala	Tyr	Arg	Met
			260					265					270		

Leu Cys Ala Ala Ser Asp Ser Gly Ala Val Leu Lys Val Ala Met Ser  
 275 280 285  
 Ser Gly Phe Ser Asp Ser Ser His Phe Ser Lys Lys Phe Lys Glu Arg  
 290 295 300  
 Tyr Gly Val Ser Pro Val Ser Leu Val Arg Gln Ala  
 305 310 315

<210> 25  
 <211> 735  
 <212> DNA  
 <213> *Pseudomonas* sp.

<220>  
 <221> CDS  
 <222> (1)..(732)  
 <223> product = "Enoyl-CoA-Hydratase" / gene = "ech"

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 1 5 10 15  
 gag cag gac gca gat gct cgc gtg ctt gtt ctg act ggt gca ggc gaa 96  
 Glu Gln Asp Ala Asp Ala Arg Val Leu Val Leu Thr Gly Ala Gly Glu  
 20 25 30  
 tcc tgg acc gcg ggc atg gac ctg aag gag tat ttc cgc gag acc gat 144  
 Ser Trp Thr Ala Gly Met Asp Leu Lys Glu Tyr Phe Arg Glu Thr Asp  
 35 40 45  
 gct ggc ccc gaa att ctg caa gag aag att cgt cgc gaa gcg tcg acc 192  
 Ala Gly Pro Glu Ile Leu Gln Glu Lys Ile Arg Arg Glu Ala Ser Thr  
 50 55 60  
 tgg cag tgg aag ctc ctg cgg atg tac acc aag ccg acc atc gcg atg 240  
 Trp Gln Trp Lys Leu Leu Arg Met Tyr Thr Lys Pro Thr Ile Ala Met  
 65 70 75 80  
 gtc aat ggc tgg tgc ttc ggc ggc ggc ttc agc ccg ctg gtg gcc tgt 288  
 Val Asn Gly Trp Cys Phe Gly Gly Gly Phe Ser Pro Leu Val Ala Cys  
 85 90 95  
 gat ctg gcc atc tgt gcc gac gag gcc acc ttt ggc ctg tcc gag atc 336  
 Asp Leu Ala Ile Cys Ala Asp Glu Ala Thr Phe Gly Leu Ser Glu Ile  
 100 105 110  
 aac tgg ggc atc ccg ccg ggc aac ctg gtg agt aag gct atg gcc gac 384  
 Asn Trp Gly Ile Pro Pro Gly Asn Leu Val Ser Lys Ala Met Ala Asp  
 115 120 125  
 acc gtg ggt cac cgc gag tcc ctt tac tac atc atg act ggc aag aca 432

Thr	Val	Gly	His	Arg	Glu	Ser	Leu	Tyr	Tyr	Ile	Met	Thr	Gly	Lys	Thr		
130						135					140						
ttt	ggc	ggt	cag	cag	gcc	gcc	aag	atg	ggg	ctt	gtg	aac	cag	agt	gtt	480	
Phe	Gly	Gly	Gln	Gln	Ala	Ala	Lys	Met	Gly	Leu	Val	Asn	Gln	Ser	Val		
145					150				155						160		
ccg	ctg	gcc	gag	ctg	cgc	agt	gtc	act	gta	gag	ctg	gct	cag	aac	ctg	528	
Pro	Leu	Ala	Glu	Leu	Arg	Ser	Val	Thr	Val	Glu	Leu	Ala	Gln	Asn	Leu		
				165				170						175			
ctg	gac	aag	aac	ccc	gta	gtg	ctg	cgt	gcc	gcc	aaa	ata	ggc	ttc	aag	576	
Leu	Asp	Lys	Asn	Pro	Val	Val	Leu	Arg	Ala	Ala	Lys	Ile	Gly	Phe	Lys		
			180					185					190				
cgt	tgc	cgc	gag	ctg	act	tgg	gag	cag	aac	gag	gac	tac	ctg	tac	gcc	624	
Arg	Cys	Arg	Glu	Leu	Thr	Trp	Glu	Gln	Asn	Glu	Asp	Tyr	Leu	Tyr	Ala		
		195					200					205					
aag	ctc	gac	caa	tcc	cgt	ttg	ctc	gat	ccg	gaa	ggc	ggt	cgc	gag	cag	672	
Lys	Leu	Asp	Gln	Ser	Arg	Leu	Leu	Asp	Pro	Glu	Gly	Gly	Arg	Glu	Gln		
	210					215					220						
ggc	atg	aag	cag	ttc	ctt	gac	gag	aaa	agc	atc	aag	ccg	ggc	ttg	cag	720	
Gly	Met	Lys	Gln	Phe	Leu	Asp	Glu	Lys	Ser	Ile	Lys	Pro	Gly	Leu	Gln		
225					230				235						240		
acc	tac	aag	cgc	tga												735	
Thr	Tyr	Lys	Arg														

<210> 26  
 <211> 244  
 <212> PRT  
 <213> Pseudomonas sp.

<400> 26																	
Met	Ser	Pro	Thr	Leu	Asn	Arg	Glu	Met	Val	Glu	Val	Leu	Glu	Val	Leu		
1				5					10					15			
Glu	Gln	Asp	Ala	Asp	Ala	Arg	Val	Leu	Val	Leu	Thr	Gly	Ala	Gly	Glu		
			20					25					30				
Ser	Trp	Thr	Ala	Gly	Met	Asp	Leu	Lys	Glu	Tyr	Phe	Arg	Glu	Thr	Asp		
		35					40					45					
Ala	Gly	Pro	Glu	Ile	Leu	Gln	Glu	Lys	Ile	Arg	Arg	Glu	Ala	Ser	Thr		
	50					55				60							
Trp	Gln	Trp	Lys	Leu	Leu	Arg	Met	Tyr	Thr	Lys	Pro	Thr	Ile	Ala	Met		
65					70					75					80		
Val	Asn	Gly	Trp	Cys	Phe	Gly	Gly	Gly	Phe	Ser	Pro	Leu	Val	Ala	Cys		
				85					90						95		

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Asp Leu Ala Ile Cys Ala Asp Glu Ala Thr Phe Gly Leu Ser Glu Ile
      100                      105                      110

Asn Trp Gly Ile Pro Pro Gly Asn Leu Val Ser Lys Ala Met Ala Asp
      115                      120                      125

Thr Val Gly His Arg Glu Ser Leu Tyr Tyr Ile Met Thr Gly Lys Thr
      130                      135                      140

Phe Gly Gly Gln Gln Ala Ala Lys Met Gly Leu Val Asn Gln Ser Val
      145                      150                      155                      160

Pro Leu Ala Glu Leu Arg Ser Val Thr Val Glu Leu Ala Gln Asn Leu
      165                      170                      175

Leu Asp Lys Asn Pro Val Val Leu Arg Ala Ala Lys Ile Gly Phe Lys
      180                      185                      190

Arg Cys Arg Glu Leu Thr Trp Glu Gln Asn Glu Asp Tyr Leu Tyr Ala
      195                      200                      205

Lys Leu Asp Gln Ser Arg Leu Leu Asp Pro Glu Gly Gly Arg Glu Gln
      210                      215                      220

Gly Met Lys Gln Phe Leu Asp Glu Lys Ser Ile Lys Pro Gly Leu Gln
      225                      230                      235                      240

Thr Tyr Lys Arg

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<210> 27
<211> 1446
<212> DNA
<213> Pseudomonas sp.

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<220>
<221> CDS
<222> (1)..(1443)
<223> product = Vanillin-Dehydrogenase" / gene = "vdh"

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Met Phe His Val Pro Leu Leu Ile Gly Gly Lys Pro Cys Ser Ala Ser
  1                      5                      10                      15

gat gag cgc acc ttc gag cgt cgt agc ccg ctg acc gga gaa gtg gta 96
Asp Glu Arg Thr Phe Glu Arg Arg Ser Pro Leu Thr Gly Glu Val Val
      20                      25                      30

tcg cgc gtc gct gct gcc agt ttg gaa gat gcg gac gcc gca gtg gcc 144
Ser Arg Val Ala Ala Ala Ser Leu Glu Asp Ala Asp Ala Ala Val Ala
      35                      40                      45

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gct gca cag gct gcg ttt cct gaa tgg gcg gcg ctt gct ccg agc gaa	192
Ala Ala Gln Ala Ala Phe Pro Glu Trp Ala Ala Leu Ala Pro Ser Glu	
50 55 60	
cgc cgt gcc cga ctg ctg cga gcg gcg gat ctt cta gag gac cgt tct	240
Arg Arg Ala Arg Leu Leu Arg Ala Ala Asp Leu Leu Glu Asp Arg Ser	
65 70 75 80	
tcc gag ttc acc gcc gca gcg agt gaa act ggc gca gcg gga aac tgg	288
Ser Glu Phe Thr Ala Ala Ser Glu Thr Gly Ala Ala Gly Asn Trp	
85 90 95	
tat ggg ttt aac gtt tac ctg gcg gcg ggc atg ttg cgg gaa gcc gcg	336
Tyr Gly Phe Asn Val Tyr Leu Ala Ala Gly Met Leu Arg Glu Ala Ala	
100 105 110	
gcc atg acc aca cag att cag ggc gat gtc att ccg tcc aat gtg ccc	384
Ala Met Thr Thr Gln Ile Gln Gly Asp Val Ile Pro Ser Asn Val Pro	
115 120 125	
ggt agc ttt gcc atg gcg gtt cga cag cca tgt ggc gtg gtg ctc ggt	432
Gly Ser Phe Ala Met Ala Val Arg Gln Pro Cys Gly Val Val Leu Gly	
130 135 140	
att gcg cct tgg aat gct ccg gta atc ctt ggc gta cgg gct gtt gcg	480
Ile Ala Pro Trp Asn Ala Pro Val Ile Leu Gly Val Arg Ala Val Ala	
145 150 155 160	
atg ccg ttg gca tgc ggc aat acc gtg gtg ttg aaa agc tct gag ctg	528
Met Pro Leu Ala Cys Gly Asn Thr Val Val Leu Lys Ser Ser Glu Leu	
165 170 175	
agt ccc ttt acc cat cgc ctg att ggt cag gtg ttg cat gat gct ggt	576
Ser Pro Phe Thr His Arg Leu Ile Gly Gln Val Leu His Asp Ala Gly	
180 185 190	
ctg ggg gat ggc gtg gtg aat gtc atc agc aat gcc ccg caa gac gct	624
Leu Gly Asp Gly Val Val Asn Val Ile Ser Asn Ala Pro Gln Asp Ala	
195 200 205	
cct gcg gtg gtg gag cga ctg att gca aat cct gcg gta cgt cga gtg	672
Pro Ala Val Val Glu Arg Leu Ile Ala Asn Pro Ala Val Arg Arg Val	
210 215 220	
aac ttc acc ggt tcg acc cac gtt gga cgg atc att ggt gag ctg tct	720
Asn Phe Thr Gly Ser Thr His Val Gly Arg Ile Ile Gly Glu Leu Ser	
225 230 235 240	
gcg cgt cat ctg aag cct gct gtg ctg gaa tta ggt ggt aag gct ccg	768
Ala Arg His Leu Lys Pro Ala Val Leu Glu Leu Gly Gly Lys Ala Pro	
245 250 255	
ttc ttg gtc ttg gac gat gcc gac ctc gat gcg gcg gtc gaa gcg gcg	816
Phe Leu Val Leu Asp Asp Ala Asp Leu Asp Ala Ala Val Glu Ala Ala	
260 265 270	

gcc ttt ggt gcc tac ttc aat cag ggt caa atc tgc atg tcc act gag	864
Ala Phe Gly Ala Tyr Phe Asn Gln Gly Gln Ile Cys Met Ser Thr Glu	
275 280 285	
cgt ctg att gtg aca gca gtc gca gac gcc ttt gtt gaa aag ctg gcg	912
Arg Leu Ile Val Thr Ala Val Ala Asp Ala Phe Val Glu Lys Leu Ala	
290 295 300	
agg aag gtc gcc aca ctg cgt gct ggc gat cct aat gat ccg caa tcg	960
Arg Lys Val Ala Thr Leu Arg Ala Gly Asp Pro Asn Asp Pro Gln Ser	
305 310 315 320	
gtc ttg ggt tcg ttg att gat gcc aat gca ggt caa cgc atc cag gtt	1008
Val Leu Gly Ser Leu Ile Asp Ala Asn Ala Gly Gln Arg Ile Gln Val	
325 330 335	
ctg gtc gat gat gcg ctc gca aaa ggc gcg cgg cag gtc gtc ggt ggt	1056
Leu Val Asp Asp Ala Leu Ala Lys Gly Ala Arg Gln Val Val Gly Gly	
340 345 350	
ggc tta gat ggc agc atc atg cag ccg atg ctg ctt gat cag gtc act	1104
Gly Leu Asp Gly Ser Ile Met Gln Pro Met Leu Leu Asp Gln Val Thr	
355 360 365	
gaa gag atg cgg ctc tac cgt gag gag tcc ttt ggc cct gtt gcc gtt	1152
Glu Glu Met Arg Leu Tyr Arg Glu Glu Ser Phe Gly Pro Val Ala Val	
370 375 380	
gtc ttg cgc ggc gat ggt gat gaa gaa ctg ctg cgt ctt gcc aac gat	1200
Val Leu Arg Gly Asp Gly Asp Glu Glu Leu Leu Arg Leu Ala Asn Asp	
385 390 395 400	
tcg gag ttt ggt ctt tcg gcc gcc att ttc agc cgt gac gtc tcg cgc	1248
Ser Glu Phe Gly Leu Ser Ala Ala Ile Phe Ser Arg Asp Val Ser Arg	
405 410 415	
gca atg gaa ttg gcc cag cgc gtc gat tcg ggc att tgc cat atc aat	1296
Ala Met Glu Leu Ala Gln Arg Val Asp Ser Gly Ile Cys His Ile Asn	
420 425 430	
gga ccg act gtg cat gac gag gct cag atg cca ttc ggt ggg gtg aag	1344
Gly Pro Thr Val His Asp Glu Ala Gln Met Pro Phe Gly Gly Val Lys	
435 440 445	
tcc agc ggc tac ggc agc ttc ggc agt cga gca tcg att gag cac ttt	1392
Ser Ser Gly Tyr Gly Ser Phe Gly Ser Arg Ala Ser Ile Glu His Phe	
450 455 460	
acc cag ctg cgc tgg ctg acc att cag aat ggc ccg cgg cac tat cca	1440
Thr Gln Leu Arg Trp Leu Thr Ile Gln Asn Gly Pro Arg His Tyr Pro	
465 470 475 480	
atc taa	1446
Ile	

<210> 28  
 <211> 481  
 <212> PRT  
 <213> Pseudomonas sp.

<400> 28

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Ser	Arg	Val	Ala	Ala	Ala	Ser	Leu	Glu	Asp	Ala	Asp	Ala	Ala	Val	Ala	35	40	45	
Ala	Ala	Gln	Ala	Ala	Phe	Pro	Glu	Trp	Ala	Ala	Leu	Ala	Pro	Ser	Glu	50	55	60	
Arg	Arg	Ala	Arg	Leu	Leu	Arg	Ala	Ala	Asp	Leu	Leu	Glu	Asp	Arg	Ser	65	70	75	80
Ser	Glu	Phe	Thr	Ala	Ala	Ala	Ser	Glu	Thr	Gly	Ala	Ala	Gly	Asn	Trp	85	90	95	
Tyr	Gly	Phe	Asn	Val	Tyr	Leu	Ala	Ala	Gly	Met	Leu	Arg	Glu	Ala	Ala	100	105	110	
Ala	Met	Thr	Thr	Gln	Ile	Gln	Gly	Asp	Val	Ile	Pro	Ser	Asn	Val	Pro	115	120	125	
Gly	Ser	Phe	Ala	Met	Ala	Val	Arg	Gln	Pro	Cys	Gly	Val	Val	Leu	Gly	130	135	140	
Ile	Ala	Pro	Trp	Asn	Ala	Pro	Val	Ile	Leu	Gly	Val	Arg	Ala	Val	Ala	145	150	155	160
Met	Pro	Leu	Ala	Cys	Gly	Asn	Thr	Val	Val	Leu	Lys	Ser	Ser	Glu	Leu	165	170	175	
Ser	Pro	Phe	Thr	His	Arg	Leu	Ile	Gly	Gln	Val	Leu	His	Asp	Ala	Gly	180	185	190	
Leu	Gly	Asp	Gly	Val	Val	Asn	Val	Ile	Ser	Asn	Ala	Pro	Gln	Asp	Ala	195	200	205	
Pro	Ala	Val	Val	Glu	Arg	Leu	Ile	Ala	Asn	Pro	Ala	Val	Arg	Arg	Val	210	215	220	
Asn	Phe	Thr	Gly	Ser	Thr	His	Val	Gly	Arg	Ile	Ile	Gly	Glu	Leu	Ser	225	230	235	240
Ala	Arg	His	Leu	Lys	Pro	Ala	Val	Leu	Glu	Leu	Gly	Gly	Lys	Ala	Pro	245	250	255	

Phe Leu Val Leu Asp Asp Ala Asp Leu Asp Ala Ala Val Glu Ala Ala  
260 265 270  
Ala Phe Gly Ala Tyr Phe Asn Gln Gly Gln Ile Cys Met Ser Thr Glu  
275 280 285  
Arg Leu Ile Val Thr Ala Val Ala Asp Ala Phe Val Glu Lys Leu Ala  
290 295 300  
Arg Lys Val Ala Thr Leu Arg Ala Gly Asp Pro Asn Asp Pro Gln Ser  
305 310 315 320  
Val Leu Gly Ser Leu Ile Asp Ala Asn Ala Gly Gln Arg Ile Gln Val  
325 330 335  
Leu Val Asp Asp Ala Leu Ala Lys Gly Ala Arg Gln Val Val Gly Gly  
340 345 350  
Gly Leu Asp Gly Ser Ile Met Gln Pro Met Leu Leu Asp Gln Val Thr  
355 360 365  
Glu Glu Met Arg Leu Tyr Arg Glu Glu Ser Phe Gly Pro Val Ala Val  
370 375 380  
Val Leu Arg Gly Asp Gly Asp Glu Glu Leu Leu Arg Leu Ala Asn Asp  
385 390 395 400  
Ser Glu Phe Gly Leu Ser Ala Ala Ile Phe Ser Arg Asp Val Ser Arg  
405 410 415  
Ala Met Glu Leu Ala Gln Arg Val Asp Ser Gly Ile Cys His Ile Asn  
420 425 430  
Gly Pro Thr Val His Asp Glu Ala Gln Met Pro Phe Gly Gly Val Lys  
435 440 445  
Ser Ser Gly Tyr Gly Ser Phe Gly Ser Arg Ala Ser Ile Glu His Phe  
450 455 460  
Thr Gln Leu Arg Trp Leu Thr Ile Gln Asn Gly Pro Arg His Tyr Pro  
465 470 475 480  
Ile

<210> 29

<211> 1770

<212> DNA

<213> Pseudomonas sp.

<220>

<221> CDS

<222> (1) .. (1767)

<223> product = "Ferulasaeure-CoA-Synthetase" / gene =

"fcs"

<400> 29

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cgt	ctc	gag	cat	tgg	gct	aag	acc	cgt	cca	gaa	caa	acc	tgc	gtt	gct	96
Arg	Leu	Glu	His	Trp	Ala	Lys	Thr	Arg	Pro	Glu	Gln	Thr	Cys	Val	Ala	
			20					25					30			
gcc	agg	gcg	gca	aat	ggg	gaa	tgg	cgt	cgt	atc	agc	tac	gcg	gaa	atg	144
Ala	Arg	Ala	Ala	Asn	Gly	Glu	Trp	Arg	Arg	Ile	Ser	Tyr	Ala	Glu	Met	
		35					40					45				
ttc	cac	aac	gtc	cgc	gcc	atc	gca	cag	agc	ttg	ctt	cct	tac	gga	cta	192
Phe	His	Asn	Val	Arg	Ala	Ile	Ala	Gln	Ser	Leu	Leu	Pro	Tyr	Gly	Leu	
	50					55					60					
tcg	gca	gag	cgt	ccg	ctg	ctt	atc	gtc	tct	gga	aat	gac	ctg	gaa	cat	240
Ser	Ala	Glu	Arg	Pro	Leu	Leu	Ile	Val	Ser	Gly	Asn	Asp	Leu	Glu	His	
65					70				75					80		
ctt	cag	ctg	gca	ttt	ggg	gct	atg	tat	gcg	ggc	att	ccc	tat	tgc	ccg	288
Leu	Gln	Leu	Ala	Phe	Gly	Ala	Met	Tyr	Ala	Gly	Ile	Pro	Tyr	Cys	Pro	
			85						90					95		
gtg	tct	cct	gct	tat	tca	ctg	ctg	tcg	caa	gat	ttg	gcg	aag	ctg	cgt	336
Val	Ser	Pro	Ala	Tyr	Ser	Leu	Leu	Ser	Gln	Asp	Leu	Ala	Lys	Leu	Arg	
			100					105					110			
cac	atc	gta	ggt	ctt	ctg	caa	ccg	gga	ctg	gtc	ttt	gct	gcc	gat	gca	384
His	Ile	Val	Gly	Leu	Leu	Gln	Pro	Gly	Leu	Val	Phe	Ala	Ala	Asp	Ala	
		115					120					125				
gca	cct	ttc	cag	cgc	gca	att	gag	acc	att	ctg	ccg	gac	gac	gtg	ccc	432
Ala	Pro	Phe	Gln	Arg	Ala	Ile	Glu	Thr	Ile	Leu	Pro	Asp	Asp	Val	Pro	
	130					135					140					
gca	atc	ttc	act	cga	ggc	gaa	ttg	gcc	ggg	cgg	cgc	acg	gtg	agt	ttt	480
Ala	Ile	Phe	Thr	Arg	Gly	Glu	Leu	Ala	Gly	Arg	Arg	Thr	Val	Ser	Phe	
145					150				155					160		
gac	agc	ctg	ctg	gag	cag	cct	ggt	ggg	att	gag	gca	gat	aat	gcc	ttt	528
Asp	Ser	Leu	Leu	Glu	Gln	Pro	Gly	Gly	Ile	Glu	Ala	Asp	Asn	Ala	Phe	
				165				170						175		
gcg	gca	act	ggc	ccc	gat	acg	att	gcc	aag	ttc	ttg	ttc	act	tct	ggc	576
Ala	Ala	Thr	Gly	Pro	Asp	Thr	Ile	Ala	Lys	Phe	Leu	Phe	Thr	Ser	Gly	
			180					185					190			
tct	acc	aaa	ctg	cct	aag	gcg	gtg	ccg	act	act	cag	cga	atg	ctc	tgc	624
Ser	Thr	Lys	Leu	Pro	Lys	Ala	Val	Pro	Thr	Thr	Gln	Arg	Met	Leu	Cys	
		195					200					205				

gcc aat cag cag atg ctt ctg caa act ttc ccg gtt ttt ggt gaa gag	672
Ala Asn Gln Gln Met Leu Leu Gln Thr Phe Pro Val Phe Gly Glu Glu	
210 215 220	
ccg ccg gtg ctg gtg gac tgg ttg ccg tgg aac cac acc ttc ggc ggc	720
Pro Pro Val Leu Val Asp Trp Leu Pro Trp Asn His Thr Phe Gly Gly	
225 230 235 240	
agc cac aac atc ggc atc gtg ttg tac aac ggc ggc acg tac tac ctt	768
Ser His Asn Ile Gly Ile Val Leu Tyr Asn Gly Gly Thr Tyr Tyr Leu	
245 250 255	
gac gac ggt aaa cca acc gcc caa ggg ttc gcc gag acg ctt cgc aac	816
Asp Asp Gly Lys Pro Thr Ala Gln Gly Phe Ala Glu Thr Leu Arg Asn	
260 265 270	
ttg agc gaa atc tct ccc act gcg tac ctc act gtg ccg aaa ggc tgg	864
Leu Ser Glu Ile Ser Pro Thr Ala Tyr Leu Thr Val Pro Lys Gly Trp	
275 280 285	
gag gaa tta gtg ggt gcc ctt gag cga gac agt acc ctg cgc gaa cgc	912
Glu Glu Leu Val Gly Ala Leu Glu Arg Asp Ser Thr Leu Arg Glu Arg	
290 295 300	
ttc ttc gct cgc atg aag ctg ttc ttc ttc gcg gcg gct ggg ttg tcg	960
Phe Phe Ala Arg Met Lys Leu Phe Phe Phe Ala Ala Ala Gly Leu Ser	
305 310 315 320	
caa ggg atc tgg gat cgt ttg gac cgg gtc gct gaa cag cac tgt ggt	1008
Gln Gly Ile Trp Asp Arg Leu Asp Arg Val Ala Glu Gln His Cys Gly	
325 330 335	
gag cgc att cgc atg atg gcg ggt ctg ggc atg acg gag act gct cct	1056
Glu Arg Ile Arg Met Met Ala Gly Leu Gly Met Thr Glu Thr Ala Pro	
340 345 350	
tcc tgc act ttt acc acc gga ccg ctg tcg atg gct ggt tac att ggg	1104
Ser Cys Thr Phe Thr Thr Gly Pro Leu Ser Met Ala Gly Tyr Ile Gly	
355 360 365	
ctg cca gcg cct ggc tgc gag gtc aag ctc gtt ccg gtc gat ggg aaa	1152
Leu Pro Ala Pro Gly Cys Glu Val Lys Leu Val Pro Val Asp Gly Lys	
370 375 380	
ttg gaa ggg cgt ttc cat ggt ccg cac gtc atg agc ggc tac tgg cgt	1200
Leu Glu Gly Arg Phe His Gly Pro His Val Met Ser Gly Tyr Trp Arg	
385 390 395 400	
gct cct gaa caa aat gcc caa gcg ttc gac gag gaa ggc tat tac tgc	1248
Ala Pro Glu Gln Asn Ala Gln Ala Phe Asp Glu Glu Gly Tyr Tyr Cys	
405 410 415	
tcc ggt gat gcc atc aaa ttg gca gat cct gcc gat cct cag aaa ggt	1296
Ser Gly Asp Ala Ile Lys Leu Ala Asp Pro Ala Asp Pro Gln Lys Gly	
420 425 430	

ctg	atg	ttt	gac	ggg	cga	att	gct	gaa	gac	ttc	aag	ctg	tcc	tca	ggg	1344
Leu	Met	Phe	Asp	Gly	Arg	Ile	Ala	Glu	Asp	Phe	Lys	Leu	Ser	Ser	Gly	
		435					440					445				

gta	ttt	gtc	agc	gtt	ggg	cca	ttg	cgc	acg	cgg	gcg	gtt	ctg	gaa	ggc	1392
Val	Phe	Val	Ser	Val	Gly	Pro	Leu	Arg	Thr	Arg	Ala	Val	Leu	Glu	Gly	
		450				455					460					

ggc	tct	tac	gtc	ctg	gac	gta	gtg	gtt	gct	gct	cct	gat	cgt	gaa	tgc	1440
Gly	Ser	Tyr	Val	Leu	Asp	Val	Val	Val	Ala	Ala	Pro	Asp	Arg	Glu	Cys	
		465			470				475						480	

ctt	gga	ttg	ctc	gtg	ttt	ccg	cgt	ctt	ctc	gac	tgc	cgt	gcc	ttg	tcg	1488
Leu	Gly	Leu	Leu	Val	Phe	Pro	Arg	Leu	Leu	Asp	Cys	Arg	Ala	Leu	Ser	
			485					490						495		

ggg	cta	gga	aaa	gag	gcg	tcg	gac	gcc	gag	gtg	ctt	gcc	agt	gag	ccg	1536
Gly	Leu	Gly	Lys	Glu	Ala	Ser	Asp	Ala	Glu	Val	Leu	Ala	Ser	Glu	Pro	
			500					505					510			

gtt	cgg	gcc	tgg	ttt	gct	gac	tgg	ctc	aaa	cga	ctc	aat	cga	gaa	gca	1584
Val	Arg	Ala	Trp	Phe	Ala	Asp	Trp	Leu	Lys	Arg	Leu	Asn	Arg	Glu	Ala	
		515					520					525				

act	ggc	aat	gcc	agt	cgc	atc	atg	tgg	gta	ggg	ctc	ctc	gat	acg	ccg	1632
Thr	Gly	Asn	Ala	Ser	Arg	Ile	Met	Trp	Val	Gly	Leu	Leu	Asp	Thr	Pro	
		530				535					540					

ccg	tcg	att	gat	aag	ggc	gag	gtc	act	gac	aag	ggc	tcg	atc	aac	cag	1680
Pro	Ser	Ile	Asp	Lys	Gly	Glu	Val	Thr	Asp	Lys	Gly	Ser	Ile	Asn	Gln	
		545			550				555						560	

cgc	gct	gtt	ttg	caa	tgg	cgg	tcg	gcg	aaa	gtt	gat	gcg	ctg	tat	cgt	1728
Arg	Ala	Val	Leu	Gln	Trp	Arg	Ser	Ala	Lys	Val	Asp	Ala	Leu	Tyr	Arg	
			565					570					575			

ggg	gaa	gat	caa	tcc	atg	ctg	cgt	gac	gag	gcc	aca	ctg	tga			1770
Gly	Glu	Asp	Gln	Ser	Met	Leu	Arg	Asp	Glu	Ala	Thr	Leu				
			580					585								

<210> 30  
 <211> 589  
 <212> PRT  
 <213> Pseudomonas sp.

<400> 30																
Met	Arg	Ser	Leu	Glu	Ala	Leu	Leu	Pro	Phe	Pro	Gly	Arg	Ile	Leu	Glu	
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Arg	Leu	Glu	His	Trp	Ala	Lys	Thr	Arg	Pro	Glu	Gln	Thr	Cys	Val	Ala	
			20					25					30			

Ala	Arg	Ala	Ala	Asn	Gly	Glu	Trp	Arg	Arg	Ile	Ser	Tyr	Ala	Glu	Met	
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	--

35					40					45					
Phe	His	Asn	Val	Arg	Ala	Ile	Ala	Gln	Ser	Leu	Leu	Pro	Tyr	Gly	Leu
50						55					60				
Ser	Ala	Glu	Arg	Pro	Leu	Leu	Ile	Val	Ser	Gly	Asn	Asp	Leu	Glu	His
65					70					75					80
Leu	Gln	Leu	Ala	Phe	Gly	Ala	Met	Tyr	Ala	Gly	Ile	Pro	Tyr	Cys	Pro
				85					90					95	
Val	Ser	Pro	Ala	Tyr	Ser	Leu	Leu	Ser	Gln	Asp	Leu	Ala	Lys	Leu	Arg
			100					105					110		
His	Ile	Val	Gly	Leu	Leu	Gln	Pro	Gly	Leu	Val	Phe	Ala	Ala	Asp	Ala
	115					120					125				
Ala	Pro	Phe	Gln	Arg	Ala	Ile	Glu	Thr	Ile	Leu	Pro	Asp	Asp	Val	Pro
	130					135					140				
Ala	Ile	Phe	Thr	Arg	Gly	Glu	Leu	Ala	Gly	Arg	Arg	Thr	Val	Ser	Phe
145					150					155					160
Asp	Ser	Leu	Leu	Glu	Gln	Pro	Gly	Gly	Ile	Glu	Ala	Asp	Asn	Ala	Phe
				165					170					175	
Ala	Ala	Thr	Gly	Pro	Asp	Thr	Ile	Ala	Lys	Phe	Leu	Phe	Thr	Ser	Gly
			180					185					190		
Ser	Thr	Lys	Leu	Pro	Lys	Ala	Val	Pro	Thr	Thr	Gln	Arg	Met	Leu	Cys
		195					200					205			
Ala	Asn	Gln	Gln	Met	Leu	Leu	Gln	Thr	Phe	Pro	Val	Phe	Gly	Glu	Glu
	210					215					220				
Pro	Pro	Val	Leu	Val	Asp	Trp	Leu	Pro	Trp	Asn	His	Thr	Phe	Gly	Gly
225					230					235					240
Ser	His	Asn	Ile	Gly	Ile	Val	Leu	Tyr	Asn	Gly	Gly	Thr	Tyr	Tyr	Leu
				245					250					255	
Asp	Asp	Gly	Lys	Pro	Thr	Ala	Gln	Gly	Phe	Ala	Glu	Thr	Leu	Arg	Asn
			260					265					270		
Leu	Ser	Glu	Ile	Ser	Pro	Thr	Ala	Tyr	Leu	Thr	Val	Pro	Lys	Gly	Trp
		275					280					285			
Glu	Glu	Leu	Val	Gly	Ala	Leu	Glu	Arg	Asp	Ser	Thr	Leu	Arg	Glu	Arg
	290					295					300				
Phe	Phe	Ala	Arg	Met	Lys	Leu	Phe	Phe	Phe	Ala	Ala	Ala	Gly	Leu	Ser
305					310					315					320
Gln	Gly	Ile	Trp	Asp	Arg	Leu	Asp	Arg	Val	Ala	Glu	Gln	His	Cys	Gly
				325					330					335	
Glu	Arg	Ile	Arg	Met	Met	Ala	Gly	Leu	Gly	Met	Thr	Glu	Thr	Ala	Pro

340	345	350
Ser Cys Thr Phe Thr Thr Gly Pro Leu Ser Met Ala Gly Tyr Ile Gly		
355	360	365
Leu Pro Ala Pro Gly Cys Glu Val Lys Leu Val Pro Val Asp Gly Lys		
370	375	380
Leu Glu Gly Arg Phe His Gly Pro His Val Met Ser Gly Tyr Trp Arg		
385	390	395
Ala Pro Glu Gln Asn Ala Gln Ala Phe Asp Glu Glu Gly Tyr Tyr Cys		
405	410	415
Ser Gly Asp Ala Ile Lys Leu Ala Asp Pro Ala Asp Pro Gln Lys Gly		
420	425	430
Leu Met Phe Asp Gly Arg Ile Ala Glu Asp Phe Lys Leu Ser Ser Gly		
435	440	445
Val Phe Val Ser Val Gly Pro Leu Arg Thr Arg Ala Val Leu Glu Gly		
450	455	460
Gly Ser Tyr Val Leu Asp Val Val Val Ala Ala Pro Asp Arg Glu Cys		
465	470	475
Leu Gly Leu Leu Val Phe Pro Arg Leu Leu Asp Cys Arg Ala Leu Ser		
485	490	495
Gly Leu Gly Lys Glu Ala Ser Asp Ala Glu Val Leu Ala Ser Glu Pro		
500	505	510
Val Arg Ala Trp Phe Ala Asp Trp Leu Lys Arg Leu Asn Arg Glu Ala		
515	520	525
Thr Gly Asn Ala Ser Arg Ile Met Trp Val Gly Leu Leu Asp Thr Pro		
530	535	540
Pro Ser Ile Asp Lys Gly Glu Val Thr Asp Lys Gly Ser Ile Asn Gln		
545	550	555
Arg Ala Val Leu Gln Trp Arg Ser Ala Lys Val Asp Ala Leu Tyr Arg		
565	570	575
Gly Glu Asp Gln Ser Met Leu Arg Asp Glu Ala Thr Leu		
580	585	

<210> 31  
 <211> 1296  
 <212> DNA  
 <213> Pseudomonas sp.

<220>  
 <221> CDS  
 <222> (1) .. (1293)

<223> product = "beta-Ketothiolase" / gene = "aat"

<400> 31

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Met Ser Trp Ser Gly Gly Ala Tyr Ser Ala Phe Ser Asp Thr Ala Leu	
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ggt gcg gca gtg cgc acc ccc tgg att gat tgc ggg ggt gcc ctg tcg	96
Val Ala Ala Val Arg Thr Pro Trp Ile Asp Cys Gly Gly Ala Leu Ser	
20 25 30	
ctg gtg tcg cct atc gac tta ggg gta aag gtc gct cgc gaa gtt ctg	144
Leu Val Ser Pro Ile Asp Leu Gly Val Lys Val Ala Arg Glu Val Leu	
35 40 45	
atg cgt gcg tcg ctt gaa cca caa atg gtc gat agc gta ctc gca ggc	192
Met Arg Ala Ser Leu Glu Pro Gln Met Val Asp Ser Val Leu Ala Gly	
50 55 60	
tct atg gct caa gca agc ttt gat gct tac ctg ctc ccg cgg cac att	240
Ser Met Ala Gln Ala Ser Phe Asp Ala Tyr Leu Leu Pro Arg His Ile	
65 70 75 80	
ggc ttg tac agc ggt gtt ccc aag tcg gtt ccg gcc ttg ggg gtg cag	288
Gly Leu Tyr Ser Gly Val Pro Lys Ser Val Pro Ala Leu Gly Val Gln	
85 90 95	
cgc att tgc ggc aca ggc ttc gaa ctg ctt cgg cag gcc ggc gag cag	336
Arg Ile Cys Gly Thr Gly Phe Glu Leu Leu Arg Gln Ala Gly Glu Gln	
100 105 110	
att tcc caa ggc gct gat cac gtg ctg tgt gtc gcg gca gag tcc atg	384
Ile Ser Gln Gly Ala Asp His Val Leu Cys Val Ala Ala Glu Ser Met	
115 120 125	
tcg cgt aac ccc atc gcg tcg tat aca cac cgg ggc ggg ttc cgc ctc	432
Ser Arg Asn Pro Ile Ala Ser Tyr Thr His Arg Gly Gly Phe Arg Leu	
130 135 140	
ggt gcg ccc gtt gag ttc aag gat ttt ttg tgg gag gca ttg ttt gat	480
Gly Ala Pro Val Glu Phe Lys Asp Phe Leu Trp Glu Ala Leu Phe Asp	
145 150 155 160	
cct gct cca gga ctc gac atg atc gct acc gca gaa aac ctg gcg cgc	528
Pro Ala Pro Gly Leu Asp Met Ile Ala Thr Ala Glu Asn Leu Ala Arg	
165 170 175	
ctg tac gga atc acc agg gga gaa gct aat tcc tac gcg gta agc agc	576
Leu Tyr Gly Ile Thr Arg Gly Glu Ala Asn Ser Tyr Ala Val Ser Ser	
180 185 190	
ttc gag cgc gca ttg agg gcg caa gag gag aaa tgg att gac caa gag	624
Phe Glu Arg Ala Leu Arg Ala Gln Glu Glu Lys Trp Ile Asp Gln Glu	
195 200 205	
atc gtg gct gtt acg gat gaa cag ttc gat tta gag ggc tac aac agt	672
Ile Val Ala Val Thr Asp Glu Gln Phe Asp Leu Glu Gly Tyr Asn Ser	

210	215	220	
cga gca att gaa ctg cct cgg aag gca aaa ttg ttg atc gtg aca gtc			720
Arg Ala Ile Glu Leu Pro Arg Lys Ala Lys Leu Leu Ile Val Thr Val			
225	230	235	240
atc cgc ggc cta gca gtc ttt gaa gcc ctt tcc cga ttg aag cct gtt			768
Ile Arg Gly Leu Ala Val Phe Glu Ala Leu Ser Arg Leu Lys Pro Val			
	245	250	255
cat tct ggc ggg gtg cag act gcg ggc aac agc tgt gcc gta gtg gac			816
His Ser Gly Gly Val Gln Thr Ala Gly Asn Ser Cys Ala Val Val Asp			
	260	265	270
ggc gcc gcg gcg gct ttg gtg gct cga gag tcg tct gcg aca cag ccg			864
Gly Ala Ala Ala Ala Leu Val Ala Arg Glu Ser Ser Ala Thr Gln Pro			
	275	280	285
gtc ttg gct agg ata ctg gct acc tcc gta gtc ggg atc gag ccc gag			912
Val Leu Ala Arg Ile Leu Ala Thr Ser Val Val Gly Ile Glu Pro Glu			
	290	295	300
cat atg ggg ctc ggc cct gcg ccc gcg att cgc ctg ctg ctt gcg cgt			960
His Met Gly Leu Gly Pro Ala Pro Ala Ile Arg Leu Leu Leu Ala Arg			
305	310	315	320
agt gat ctt agt ttg agg gat atc gac ctc ttt gag ata aac gag gcg			1008
Ser Asp Leu Ser Leu Arg Asp Ile Asp Leu Phe Glu Ile Asn Glu Ala			
	325	330	335
cag gcc gcc caa gtt cta gcg gta cag cat gaa ttg ggt att gag cac			1056
Gln Ala Ala Gln Val Leu Ala Val Gln His Glu Leu Gly Ile Glu His			
	340	345	350
tca aaa ctt aat att tgg ggc ggg gcc att gca ctt gga cac ccg ctt			1104
Ser Lys Leu Asn Ile Trp Gly Gly Ala Ile Ala Leu Gly His Pro Leu			
	355	360	365
gcc gcg acc gga ttg cgt ctc tgc atg acc ctc gct cac caa ttg caa			1152
Ala Ala Thr Gly Leu Arg Leu Cys Met Thr Leu Ala His Gln Leu Gln			
	370	375	380
gct aat aac ttt cga tat gga att gcc tcg gca tgc att ggt ggg gga			1200
Ala Asn Asn Phe Arg Tyr Gly Ile Ala Ser Ala Cys Ile Gly Gly Gly			
385	390	395	400
cag ggg atg gcg gtt ctt tta gag aat ccc cac ttc ggt tcg tcc tct			1248
Gln Gly Met Ala Val Leu Leu Glu Asn Pro His Phe Gly Ser Ser Ser			
	405	410	415
gca cga agt tcg atg att aac aga gtt gac cac tat cca ctg agc taa			1296
Ala Arg Ser Ser Met Ile Asn Arg Val Asp His Tyr Pro Leu Ser			
	420	425	430

<210> 32  
<211> 431  
<212> PRT  
<213> Pseudomonas sp.

<400> 32

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Val	Ala	Ala	Val	Arg	Thr	Pro	Trp	Ile	Asp	Cys	Gly	Gly	Ala	Leu	Ser
			20					25					30		
Leu	Val	Ser	Pro	Ile	Asp	Leu	Gly	Val	Lys	Val	Ala	Arg	Glu	Val	Leu
		35					40					45			
Met	Arg	Ala	Ser	Leu	Glu	Pro	Gln	Met	Val	Asp	Ser	Val	Leu	Ala	Gly
	50					55					60				
Ser	Met	Ala	Gln	Ala	Ser	Phe	Asp	Ala	Tyr	Leu	Leu	Pro	Arg	His	Ile
	65				70					75					80
Gly	Leu	Tyr	Ser	Gly	Val	Pro	Lys	Ser	Val	Pro	Ala	Leu	Gly	Val	Gln
				85					90					95	
Arg	Ile	Cys	Gly	Thr	Gly	Phe	Glu	Leu	Leu	Arg	Gln	Ala	Gly	Glu	Gln
			100					105					110		
Ile	Ser	Gln	Gly	Ala	Asp	His	Val	Leu	Cys	Val	Ala	Ala	Glu	Ser	Met
		115					120					125			
Ser	Arg	Asn	Pro	Ile	Ala	Ser	Tyr	Thr	His	Arg	Gly	Gly	Phe	Arg	Leu
	130					135					140				
Gly	Ala	Pro	Val	Glu	Phe	Lys	Asp	Phe	Leu	Trp	Glu	Ala	Leu	Phe	Asp
145					150					155					160
Pro	Ala	Pro	Gly	Leu	Asp	Met	Ile	Ala	Thr	Ala	Glu	Asn	Leu	Ala	Arg
				165					170					175	
Leu	Tyr	Gly	Ile	Thr	Arg	Gly	Glu	Ala	Asn	Ser	Tyr	Ala	Val	Ser	Ser
			180					185					190		
Phe	Glu	Arg	Ala	Leu	Arg	Ala	Gln	Glu	Glu	Lys	Trp	Ile	Asp	Gln	Glu
		195					200					205			
Ile	Val	Ala	Val	Thr	Asp	Glu	Gln	Phe	Asp	Leu	Glu	Gly	Tyr	Asn	Ser
	210					215					220				
Arg	Ala	Ile	Glu	Leu	Pro	Arg	Lys	Ala	Lys	Leu	Leu	Ile	Val	Thr	Val
225					230					235					240
Ile	Arg	Gly	Leu	Ala	Val	Phe	Glu	Ala	Leu	Ser	Arg	Leu	Lys	Pro	Val
			245						250					255	
His	Ser	Gly	Gly	Val	Gln	Thr	Ala	Gly	Asn	Ser	Cys	Ala	Val	Val	Asp
			260					265					270		

Gly Ala Ala Ala Ala Leu Val Ala Arg Glu Ser Ser Ala Thr Gln Pro  
 275 280 285  
 Val Leu Ala Arg Ile Leu Ala Thr Ser Val Val Gly Ile Glu Pro Glu  
 290 295 300  
 His Met Gly Leu Gly Pro Ala Pro Ala Ile Arg Leu Leu Leu Ala Arg  
 305 310 315 320  
 Ser Asp Leu Ser Leu Arg Asp Ile Asp Leu Phe Glu Ile Asn Glu Ala  
 325 330 335  
 Gln Ala Ala Gln Val Leu Ala Val Gln His Glu Leu Gly Ile Glu His  
 340 345 350  
 Ser Lys Leu Asn Ile Trp Gly Gly Ala Ile Ala Leu Gly His Pro Leu  
 355 360 365  
 Ala Ala Thr Gly Leu Arg Leu Cys Met Thr Leu Ala His Gln Leu Gln  
 370 375 380  
 Ala Asn Asn Phe Arg Tyr Gly Ile Ala Ser Ala Cys Ile Gly Gly Gly  
 385 390 395 400  
 Gln Gly Met Ala Val Leu Leu Glu Asn Pro His Phe Gly Ser Ser Ser  
 405 410 415  
 Ala Arg Ser Ser Met Ile Asn Arg Val Asp His Tyr Pro Leu Ser  
 420 425 430

<210> 33

<211> 1596

<212> DNA

<213> Pseudomonas sp.

<220>

<221> CDS

<222> (1)..(1593)

<223> product = "Chemotaxis-Protein" / gene = "mac"

<400> 33

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 Met Ile Ser Phe Ala Arg Met Ala Glu Ser Leu Gly Val Gln Ala Lys  
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ctt gcc ctt gcc ttc gca ctc gta tta tgt gtc ggg ctg att gtt acc 96  
 Leu Ala Leu Ala Phe Ala Leu Val Leu Cys Val Gly Leu Ile Val Thr  
 20 25 30

ggc acg ggt ttc tac agt gta cat acc ttg tca ggg ttg gtg gaa aag 144  
 Gly Thr Gly Phe Tyr Ser Val His Thr Leu Ser Gly Leu Val Glu Lys  
 35 40 45

agc gcg ata gct ggt gag ttg cgg gcg aaa att cag gaa ctg aag gtt 192  
 Ser Ala Ile Ala Gly Glu Leu Arg Ala Lys Ile Gln Glu Leu Lys Val

50	55	60	
ctg gag cag cgc gcc tta ttc atc gcc gat gaa ggg tcg ctg aag cag			240
Leu Glu Gln Arg Ala Leu Phe Ile Ala Asp Glu Gly Ser Leu Lys Gln			
65	70	75	80
cgc tcg atc ctc cta agt cag gtg ata gct gaa gtt aat gat gct ata			288
Arg Ser Ile Leu Leu Ser Gln Val Ile Ala Glu Val Asn Asp Ala Ile			
	85	90	95
gat att ttt gac ttt cag cgc gga cga tct gag tta ctt aaa ttc gct			336
Asp Ile Phe Asp Phe Gln Arg Gly Arg Ser Glu Leu Leu Lys Phe Ala			
	100	105	110
gct tct tcg cgc gaa gca agt tac tcc att gag gtc ggt agt aac gct			384
Ala Ser Ser Arg Glu Ala Ser Tyr Ser Ile Glu Val Gly Ser Asn Ala			
	115	120	125
gcg gcc gat aag ttg cag tcg ggc gaa cca agt gac gca ttg atg gtt			432
Ala Ala Asp Lys Leu Gln Ser Gly Glu Pro Ser Asp Ala Leu Met Val			
	130	135	140
gcc gat aaa aag ctg aat gtt gag tat gag caa ttg agt tct gct gtg			480
Ala Asp Lys Lys Leu Val Glu Tyr Glu Gln Leu Ser Ser Ala Val			
	145	150	155
aat gca ctg atg ggg cat tta att gag gat cag aat gaa aaa gtt cca			528
Asn Ala Leu Met Gly His Leu Ile Glu Asp Gln Asn Glu Lys Val Pro			
	165	170	175
cta atc tac tat atg ctt ggc ggc gta act ttg ttt acg atg ctc atg			576
Leu Ile Tyr Tyr Met Leu Gly Gly Val Thr Leu Phe Thr Met Leu Met			
	180	185	190
agt gct tat tcg gtc tgg ttc att tcg cgt cag tta gtt ccg cca tta			624
Ser Ala Tyr Ser Val Trp Phe Ile Ser Arg Gln Leu Val Pro Pro Leu			
	195	200	205
aag tcg acg gtg cag ctt gcc gag cgg att gca tca ggc gac ttg gct			672
Lys Ser Thr Val Gln Leu Ala Glu Arg Ile Ala Ser Gly Asp Leu Ala			
	210	215	220
gat gtc ggg gac agc agg cgc aag gat gaa atc ggt cag ttg caa agt			720
Asp Val Gly Asp Ser Arg Arg Lys Asp Glu Ile Gly Gln Leu Gln Ser			
	225	230	235
gca act agg cgg atg gcg att gga ctg cgt aat ctg gtc ggt gat att			768
Ala Thr Arg Arg Met Ala Ile Gly Leu Arg Asn Leu Val Gly Asp Ile			
	245	250	255
ggt caa agt cgt gcg caa ctg gtt tca tcg tcc agc gac ctt tcg gcc			816
Gly Gln Ser Arg Ala Gln Leu Val Ser Ser Ser Ser Asp Leu Ser Ala			
	260	265	270
atc tgt gct cag gct cag att gat gtc gag tgc cag aag ctt tcg gtc			864

Ile Cys Ala Gln Ala Gln Ile Asp Val Glu Cys Gln Lys Leu Ser Val	
275 280 285	
gcc cag gtc tct acc gcc gtg aac gag ttg gtt gaa acc gtc cag gca	912
Ala Gln Val Ser Thr Ala Val Asn Glu Leu Val Glu Thr Val Gln Ala	
290 295 300	
ata gca aaa agc acc gaa gag gca gca aca gtc gcc gtc ttg gcc gat	960
Ile Ala Lys Ser Thr Glu Glu Ala Ala Thr Val Ala Val Leu Ala Asp	
305 310 315 320	
gaa aag gca cgc ggt ggt gaa agt gtc gtt aac aag gcc gtt gat ttc	1008
Glu Lys Ala Arg Gly Gly Glu Ser Val Val Asn Lys Ala Val Asp Phe	
325 330 335	
att gag cac ctc tcc gga gat atg gcg gaa ctg gga gac gca atg gag	1056
Ile Glu His Leu Ser Gly Asp Met Ala Glu Leu Gly Asp Ala Met Glu	
340 345 350	
cgg ctt cag aac gac agt gcg cag atc aat aag gta gta gac gtc att	1104
Arg Leu Gln Asn Asp Ser Ala Gln Ile Asn Lys Val Val Asp Val Ile	
355 360 365	
aag gct gtg gcg gag cag acc aat ctg cta gcc ctg aat gcg gcg ata	1152
Lys Ala Val Ala Glu Gln Thr Asn Leu Leu Ala Leu Asn Ala Ala Ile	
370 375 380	
gag gcg gcc cgt gca gga gag cag gcc agg gcc ttt gcg gtc gtg gcg	1200
Glu Ala Ala Arg Ala Gly Glu Gln Gly Arg Gly Phe Ala Val Val Ala	
385 390 395 400	
gat gag gtt cgt gct ttg gcg atg cgc acc caa caa tcg acc aaa gaa	1248
Asp Glu Val Arg Ala Leu Ala Met Arg Thr Gln Gln Ser Thr Lys Glu	
405 410 415	
att gag agg cta gtg gtt tca ttg cag cag gga agt gaa gct gcg ggc	1296
Ile Glu Arg Leu Val Val Ser Leu Gln Gln Gly Ser Glu Ala Ala Gly	
420 425 430	
gag ttg atg cgg cgt ggc aag gtc cgg acg cat gac gtc gtt gga ttg	1344
Glu Leu Met Arg Arg Gly Lys Val Arg Thr His Asp Val Val Gly Leu	
435 440 445	
gcc cag caa gcc gcg cgc cgc gct act cga aat tac cca gct gtc gcc	1392
Ala Gln Gln Ala Ala Arg Arg Ala Thr Arg Asn Tyr Pro Ala Val Ala	
450 455 460	
ggc atc caa gcg atg aac tat cag atc gcc gct gga gca gag cag caa	1440
Gly Ile Gln Ala Met Asn Tyr Gln Ile Ala Ala Gly Ala Glu Gln Gln	
465 470 475 480	
ggg gct gct gtg gtt caa atc aac cag aat atg ctt gaa gtg cat aag	1488
Gly Ala Ala Val Val Gln Ile Asn Gln Asn Met Leu Glu Val His Lys	
485 490 495	



Lys Ser Thr Val Gln Leu Ala Glu Arg Ile Ala Ser Gly Asp Leu Ala  
 210 215 220  
 Asp Val Gly Asp Ser Arg Arg Lys Asp Glu Ile Gly Gln Leu Gln Ser  
 225 230 235 240  
 Ala Thr Arg Arg Met Ala Ile Gly Leu Arg Asn Leu Val Gly Asp Ile  
 245 250 255  
 Gly Gln Ser Arg Ala Gln Leu Val Ser Ser Ser Ser Asp Leu Ser Ala  
 260 265 270  
 Ile Cys Ala Gln Ala Gln Ile Asp Val Glu Cys Gln Lys Leu Ser Val  
 275 280 285  
 Ala Gln Val Ser Thr Ala Val Asn Glu Leu Val Glu Thr Val Gln Ala  
 290 295 300  
 Ile Ala Lys Ser Thr Glu Glu Ala Ala Thr Val Ala Val Leu Ala Asp  
 305 310 315 320  
 Glu Lys Ala Arg Gly Gly Glu Ser Val Val Asn Lys Ala Val Asp Phe  
 325 330 335  
 Ile Glu His Leu Ser Gly Asp Met Ala Glu Leu Gly Asp Ala Met Glu  
 340 345 350  
 Arg Leu Gln Asn Asp Ser Ala Gln Ile Asn Lys Val Val Asp Val Ile  
 355 360 365  
 Lys Ala Val Ala Glu Gln Thr Asn Leu Leu Ala Leu Asn Ala Ala Ile  
 370 375 380  
 Glu Ala Ala Arg Ala Gly Glu Gln Gly Arg Gly Phe Ala Val Val Ala  
 385 390 395 400  
 Asp Glu Val Arg Ala Leu Ala Met Arg Thr Gln Gln Ser Thr Lys Glu  
 405 410 415  
 Ile Glu Arg Leu Val Val Ser Leu Gln Gln Gly Ser Glu Ala Ala Gly  
 420 425 430  
 Glu Leu Met Arg Arg Gly Lys Val Arg Thr His Asp Val Val Gly Leu  
 435 440 445  
 Ala Gln Gln Ala Ala Arg Arg Ala Thr Arg Asn Tyr Pro Ala Val Ala  
 450 455 460  
 Gly Ile Gln Ala Met Asn Tyr Gln Ile Ala Ala Gly Ala Glu Gln Gln  
 465 470 475 480  
 Gly Ala Ala Val Val Gln Ile Asn Gln Asn Met Leu Glu Val His Lys  
 485 490 495  
 Met Ala Asp Glu Ser Ala Ile Lys Ala Gly Gln Thr Met Lys Ser Ser  
 500 505 510

Lys Glu Leu Ala His Leu Gly Ser Ala Leu Gln Lys Ser Val Asp Arg  
515 520 525

Phe Gln Leu  
530

<210> 35  
<211> 411  
<212> DNA  
<213> Pseudomonas sp.

<400> 35  
ctagcctaac tgttgcgctt caggctccgc atggatcttg tgcagcagca atagcaattg 60  
ttcacgttcg tcatcactca gcatcgacgt cgcgtcttgg tcgctctgta ccacgatctt 120  
cttcagctct ttgagctgcy tctccccagc tttgctgaga aatatcccat aggaacgctt 180  
gtccggcttg cagcgcacgc gcacagcaag gccgagcttc tcgagcttgt tcagcaaggg 240  
aaccagttgt ggtggttcga ttgcgagcat ccgcgctagg tcagcctgca taagcccagg 300  
gctcgcttcg atgattagaa gtgccgacag ctgcgccggg cgtaggtcat atggcgctcag 360  
ggcttcaatc aggccctgag cgagcttcag ctgtgagccg gcgtaaggca t 411

<210> 36  
<211> 136  
<212> PRT  
<213> Pseudomonas sp.

<400> 36  
Met Pro Tyr Ala Gly Ser Gln Leu Lys Leu Ala Gln Gly Leu Ile Glu  
1 5 10 15  
Ala Leu Thr Pro Tyr Asp Leu Arg Pro Ala Gln Leu Ser Ala Leu Leu  
20 25 30  
Ile Ile Glu Ala Ser Pro Gly Leu Met Gln Ala Asp Leu Ala Arg Met  
35 40 45  
Leu Ala Ile Glu Pro Pro Gln Leu Val Pro Leu Leu Asn Lys Leu Glu  
50 55 60  
Lys Leu Gly Leu Ala Val Arg Val Arg Cys Lys Pro Asp Lys Arg Ser  
65 70 75 80  
Tyr Gly Ile Phe Leu Ser Lys Ala Gly Glu Thr Gln Leu Lys Glu Leu  
85 90 95  
Lys Lys Ile Val Val Gln Ser Asp Gln Asp Ala Thr Ser Met Leu Ser  
100 105 110

Asp Asp Glu Arg Glu Gln Leu Leu Leu Leu Leu His Lys Ile His Ala  
115 120 125

Glu Pro Glu Ala Gln Gln Leu Gly  
130 135

<210> 37

<211> 1446

<212> DNA

<213> Pseudomonas sp.

<220>

<221> CDS

<222> (1)..(1443)

<223> product = "Coniferylaldehyd-Dehydrogenase" / gene  
= "caldh"

<400> 37

atg agc att ctt ggt ttg aat ggt gcc ccg gtc gga gct gag cag ctg	48
Met Ser Ile Leu Gly Leu Asn Gly Ala Pro Val Gly Ala Glu Gln Leu	
1 5 10 15	
ggc tcg gct ctt gat cgc atg aag aag gcg cac ctg gag cag ggg cct	96
Gly Ser Ala Leu Asp Arg Met Lys Lys Ala His Leu Glu Gln Gly Pro	
20 25 30	
gca aac ttg gag ctg cgt ctg agt agg ctg gat cgt gcg att gca atg	144
Ala Asn Leu Glu Leu Arg Leu Ser Arg Leu Asp Arg Ala Ile Ala Met	
35 40 45	
ctt ctg gaa aat cgt gaa gca att gcc gac gcg gtt tct gct gac ttt	192
Leu Leu Glu Asn Arg Glu Ala Ile Ala Asp Ala Val Ser Ala Asp Phe	
50 55 60	
ggc aat cgc agc cgt gag caa aca ctg ctt tgc gac att gct ggc tcg	240
Gly Asn Arg Ser Arg Glu Gln Thr Leu Leu Cys Asp Ile Ala Gly Ser	
65 70 75 80	
gtg gca agc ctg aag gat agc cgc gag cac gtg gcc aaa tgg atg gag	288
Val Ala Ser Leu Lys Asp Ser Arg Glu His Val Ala Lys Trp Met Glu	
85 90 95	
ccc gaa cat cac aag gcg atg ttt cca ggg gcg gag gca cgc gtt gag	336
Pro Glu His His Lys Ala Met Phe Pro Gly Ala Glu Ala Arg Val Glu	
100 105 110	
ttt cag ccg ctg ggt gtc gtt ggg gtc att agt ccc tgg aac ttc cct	384
Phe Gln Pro Leu Gly Val Val Gly Val Ile Ser Pro Trp Asn Phe Pro	
115 120 125	
atc gta ctg gcc ttt ggg ccg ctg gcc ggc ata ttc gca gca ggt aat	432
Ile Val Leu Ala Phe Gly Pro Leu Ala Gly Ile Phe Ala Ala Gly Asn	
130 135 140	

cgc gcc atg ctc aag ccg tcc gag ctt acc ccg cgg act tct gcc ctg	480
Arg Ala Met Leu Lys Pro Ser Glu Leu Thr Pro Arg Thr Ser Ala Leu	
145 150 155 160	
ctt gcg gag cta att gct cgt tac ttc gat gaa act gag ctg act aca	528
Leu Ala Glu Leu Ile Ala Arg Tyr Phe Asp Glu Thr Glu Leu Thr Thr	
165 170 175	
gtg ctg ggc gac gct gaa gtc ggt gcg ctg ttc agt gct cag cct ttc	576
Val Leu Gly Asp Ala Glu Val Gly Ala Leu Phe Ser Ala Gln Pro Phe	
180 185 190	
gat cat ctg atc ttc acc ggc ggc act gcc gtg gcc aag cac atc atg	624
Asp His Leu Ile Phe Thr Gly Gly Thr Ala Val Ala Lys His Ile Met	
195 200 205	
cgt gcc gcg gcg gat aac cta gtg ccc gtt acc ctg gaa ttg ggt ggc	672
Arg Ala Ala Ala Asp Asn Leu Val Pro Val Thr Leu Glu Leu Gly Gly	
210 215 220	
aaa tcg ccg gtg atc gtt tcc cgc agt gca gat atg gcg gac gtt gca	720
Lys Ser Pro Val Ile Val Ser Arg Ser Ala Asp Met Ala Asp Val Ala	
225 230 235 240	
caa cgg gtg ttg acg gtg aaa acc ttc aat gcc ggg caa atc tgt ctg	768
Gln Arg Val Leu Thr Val Lys Thr Phe Asn Ala Gly Gln Ile Cys Leu	
245 250 255	
gca ccg gac tat gtg ctg ctg ccg gaa gaa tcg ctg gat agc ttt gtc	816
Ala Pro Asp Tyr Val Leu Leu Pro Glu Glu Ser Leu Asp Ser Phe Val	
260 265 270	
gcc gag gcg acg cgc ttc gtg gcc gca atg tat ccc tcg ctt cta gat	864
Ala Glu Ala Thr Arg Phe Val Ala Ala Met Tyr Pro Ser Leu Leu Asp	
275 280 285	
aat ccg gat tac acg tcg atc atc aat gcc cga aat ttc gac cgt ctg	912
Asn Pro Asp Tyr Thr Ser Ile Ile Asn Ala Arg Asn Phe Asp Arg Leu	
290 295 300	
cat cgc tac ctg act gat gcg cag gca aag gga ggg cgc gtc att gaa	960
His Arg Tyr Leu Thr Asp Ala Gln Ala Lys Gly Gly Arg Val Ile Glu	
305 310 315 320	
atc aat cct gcg gcc gaa gag ttg ggg gat agt ggt atc agg aag atc	1008
Ile Asn Pro Ala Ala Glu Glu Leu Gly Asp Ser Gly Ile Arg Lys Ile	
325 330 335	
gcg ccc act ttg atc gtg aat gtg tcg gat gaa atg ctg gtc ttg aac	1056
Ala Pro Thr Leu Ile Val Asn Val Ser Asp Glu Met Leu Val Leu Asn	
340 345 350	
gag gag atc ttt ggt ccg ctg ctc ccg atc aag act tat cgt gat ttc	1104
Glu Glu Ile Phe Gly Pro Leu Leu Pro Ile Lys Thr Tyr Arg Asp Phe	
355 360 365	

gac tcg gct atc gac tac gtc aac agc aag cag cga cca ctt gcc tcg 1152  
 Asp Ser Ala Ile Asp Tyr Val Asn Ser Lys Gln Arg Pro Leu Ala Ser  
 370 375 380

tac ttc ttc ggc gaa gat gcg gtt gag cgt gag caa gtg ctt aag cgt 1200  
 Tyr Phe Phe Gly Glu Asp Ala Val Glu Arg Glu Gln Val Leu Lys Arg  
 385 390 395 400

acg gtt tcg ggc gcc gtg gtc gtg aac gat gtc atg agc cat gtg atg 1248  
 Thr Val Ser Gly Ala Val Val Val Asn Asp Val Met Ser His Val Met  
 405 410 415

atg gat acg ctt cca ttt ggt ggt gtg ggg cac tcg ggg atg ggg gca 1296  
 Met Asp Thr Leu Pro Phe Gly Gly Val Gly His Ser Gly Met Gly Ala  
 420 425 430

tat cac ggc att tat ggt ttc cga acc ttc agc cat gcc aag cct gtt 1344  
 Tyr His Gly Ile Tyr Gly Phe Arg Thr Phe Ser His Ala Lys Pro Val  
 435 440 445

ctc gtg caa agt cct gtg ggt gag tcg aac ttg gcg atg cgc gca ccc 1392  
 Leu Val Gln Ser Pro Val Gly Glu Ser Asn Leu Ala Met Arg Ala Pro  
 450 455 460

tac gga gaa gcg atc cac gga ctg ctc tct gtc ctc ctt tca acg gag 1440  
 Tyr Gly Glu Ala Ile His Gly Leu Leu Ser Val Leu Leu Ser Thr Glu  
 465 470 475 480

tgt tag 1446  
 Cys

<210> 38  
 <211> 481  
 <212> PRT  
 <213> Pseudomonas sp.

<400> 38  
 Met Ser Ile Leu Gly Leu Asn Gly Ala Pro Val Gly Ala Glu Gln Leu  
 1 5 10 15

Gly Ser Ala Leu Asp Arg Met Lys Lys Ala His Leu Glu Gln Gly Pro  
 20 25 30

Ala Asn Leu Glu Leu Arg Leu Ser Arg Leu Asp Arg Ala Ile Ala Met  
 35 40 45

Leu Leu Glu Asn Arg Glu Ala Ile Ala Asp Ala Val Ser Ala Asp Phe  
 50 55 60

Gly Asn Arg Ser Arg Glu Gln Thr Leu Leu Cys Asp Ile Ala Gly Ser  
 65 70 75 80

Val Ala Ser Leu Lys Asp Ser Arg Glu His Val Ala Lys Trp Met Glu  
 85 90 95

Pro Glu His His Lys Ala Met Phe Pro Gly Ala Glu Ala Arg Val Glu

100						105						110					
Phe	Gln	Pro	Leu	Gly	Val	Val	Gly	Val	Ile	Ser	Pro	Trp	Asn	Phe	Pro		
115						120						125					
Ile	Val	Leu	Ala	Phe	Gly	Pro	Leu	Ala	Gly	Ile	Phe	Ala	Ala	Gly	Asn		
130						135						140					
Arg	Ala	Met	Leu	Lys	Pro	Ser	Glu	Leu	Thr	Pro	Arg	Thr	Ser	Ala	Leu		
145						150						155					
Leu	Ala	Glu	Leu	Ile	Ala	Arg	Tyr	Phe	Asp	Glu	Thr	Glu	Leu	Thr	Thr		
			165						170								
Val	Leu	Gly	Asp	Ala	Glu	Val	Gly	Ala	Leu	Phe	Ser	Ala	Gln	Pro	Phe		
			180						185			190					
Asp	His	Leu	Ile	Phe	Thr	Gly	Gly	Thr	Ala	Val	Ala	Lys	His	Ile	Met		
195						200						205					
Arg	Ala	Ala	Ala	Asp	Asn	Leu	Val	Pro	Val	Thr	Leu	Glu	Leu	Gly	Gly		
210						215						220					
Lys	Ser	Pro	Val	Ile	Val	Ser	Arg	Ser	Ala	Asp	Met	Ala	Asp	Val	Ala		
225						230						235					
Gln	Arg	Val	Leu	Thr	Val	Lys	Thr	Phe	Asn	Ala	Gly	Gln	Ile	Cys	Leu		
			245						250			255					
Ala	Pro	Asp	Tyr	Val	Leu	Leu	Pro	Glu	Glu	Ser	Leu	Asp	Ser	Phe	Val		
			260						265			270					
Ala	Glu	Ala	Thr	Arg	Phe	Val	Ala	Ala	Met	Tyr	Pro	Ser	Leu	Leu	Asp		
275						280						285					
Asn	Pro	Asp	Tyr	Thr	Ser	Ile	Ile	Asn	Ala	Arg	Asn	Phe	Asp	Arg	Leu		
290						295						300					
His	Arg	Tyr	Leu	Thr	Asp	Ala	Gln	Ala	Lys	Gly	Gly	Arg	Val	Ile	Glu		
305						310						315					
Ile	Asn	Pro	Ala	Ala	Glu	Glu	Leu	Gly	Asp	Ser	Gly	Ile	Arg	Lys	Ile		
			325						330			335					
Ala	Pro	Thr	Leu	Ile	Val	Asn	Val	Ser	Asp	Glu	Met	Leu	Val	Leu	Asn		
			340						345			350					
Glu	Glu	Ile	Phe	Gly	Pro	Leu	Leu	Pro	Ile	Lys	Thr	Tyr	Arg	Asp	Phe		
355						360						365					
Asp	Ser	Ala	Ile	Asp	Tyr	Val	Asn	Ser	Lys	Gln	Arg	Pro	Leu	Ala	Ser		
370						375						380					
Tyr	Phe	Phe	Gly	Glu	Asp	Ala	Val	Glu	Arg	Glu	Gln	Val	Leu	Lys	Arg		
385						390						395					
Thr	Val	Ser	Gly	Ala	Val	Val	Val	Asn	Asp	Val	Met	Ser	His	Val	Met		

	405		410		415										
Met	Asp	Thr	Leu	Pro	Phe	Gly	Gly	Val	Gly	His	Ser	Gly	Met	Gly	Ala
			420					425					430		
Tyr	His	Gly	Ile	Tyr	Gly	Phe	Arg	Thr	Phe	Ser	His	Ala	Lys	Pro	Val
		435					440					445			
Leu	Val	Gln	Ser	Pro	Val	Gly	Glu	Ser	Asn	Leu	Ala	Met	Arg	Ala	Pro
		450				455					460				
Tyr	Gly	Glu	Ala	Ile	His	Gly	Leu	Leu	Ser	Val	Leu	Leu	Ser	Thr	Glu
465					470					475					480
Cys															

<210> 39  
 <211> 1827  
 <212> DNA  
 <213> Pseudomonas sp.

<400> 39  
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 ccggcgggca gcttccgaga cattgccttt cacctggccc agagcatggc taatcatcgc 120  
 gtctccact tcttgcagcg tcatcgcgct caggctcttt gagtcaagcg gcgagtcgat 180  
 tgtgtgggtc ggtttgaga aggaagtact tgggctgcca gtttcctgtg gctgattatc 240  
 ttgagcgggtg gccaggatgc cgctggcccc aatggagaac atcggttgag tcagtcgttc 300  
 accgctagtg aagaggtggc tcacgtcaat ggctccatcc tccggagcgc tgatgactcc 360  
 gcgctccacc aaattttgaa gctcccggat gtttcctgga aagtcgtagc caagcagggc 420  
 attggctgca cgtggagtga atccgctgac caccgggcta tgacgctgat tgaagcgggtg 480  
 caggaaatag gtcattcagga ggggaatgtc ttccttcctc tctcgaagcg gcgggaggtg 540  
 gatcgggtaa acattgaggc ggaaaaaag gtcctcgcgg aactcgccgc gctggacgcc 600  
 tgcgcgaaga tcgacattgg ttgcggctac cacacggacg tcaaccttga gtgtcctgct 660  
 tccgccaaacc cgttcgacct ccgactcttg cagggcgcga agtaacttcc cttggggccac 720  
 gaggcttagc gtccctatct cgtcaaggaa tagtgtgcg cccgaagcgc gctcgaaccg 780  
 tcctgctcga gattgggtgg cgccggtaaa cgcctccgtc tcgacgccga acaactcgga 840  
 ctccatcagg gtttcgggaa tacgtgcgca attgaccgca acaaacgggc cgctcgtgtct 900

ggggctgatg cgggtgaagca tgcgggagaa catctccttg cccacacctg attcaccctg 960  
 aaacagtacc gtcgcctccg tgggtgctac gcgcttcagc atgtggcagg cagcattgaa 1020  
 tgccgaggaa attcccacca tgtcgtgttc cgatgcagtg cttgagtctg cggcggagtg 1080  
 atggggagtg ttcctttgtc cctgctgcgt tcttcgtctc tgcggcgtgc ttggttgccg 1140  
 acaaattggtt gcgctaagcg ccgccaagtc ctcttcggcg tcttcccatt cttccgctgg 1200  
 cttgccgatc atgcggcaga tctgcgaacc cgtggagcgg cattccacct ctcggtaaag 1260  
 gatgaggcga ccaaccagcg cggacgtata gccaatggca taaccctgtc gcgtccagca 1320  
 cgcgggctcg gtgccgatgc cgtagtgcg aatatgttca tcatcttcgc tcgaatggtg 1380  
 ccagaggaat tcgccgtagt aggtcccaa atccatgtcg aagtcgaagt ggatcggctc 1440  
 cacgcgtact gcgccttcca gagagtgcaa gttcggggccg gcggcaaata gggagagcgg 1500  
 atcggcgctt ctgaagcgct ccttcagaag ggcggcatct ttggcgccgc agtggttaacc 1560  
 ggcttcgcagc atgattccgc gggcgcgggc gaagcccacg ctttcaatta attcgcgtcg 1620  
 caatgcaccc agtccgctgc tgtggaggag cagcattcgc gcgccgttca accagatgcg 1680  
 tccatcgcca gggctgaaaa ggagggattc agtgaggtca tgaagggagg ggacggcgcc 1740  
 tggctccaat tgctcgatgg cgccgcgatt gagtgtcttg ggcgcggtct tggagagttc 1800  
 ggctagggag ataaatttgc tggccat 1827

<210> 40  
 <211> 608  
 <212> PRT  
 <213> *Pseudomonas* sp.

<400> 40  
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 Lys Thr Leu Asn Arg Gly Ala Ile Glu Gln Leu Glu Pro Gly Ala Val  
 20 25 30  
 Pro Ser Leu His Asp Leu Thr Glu Ser Leu Leu Phe Ser Pro Gly Asp  
 35 40 45  
 Gly Arg Ile Trp Leu Asn Gly Ala Arg Met Leu Leu Leu His Ser Ser  
 50 55 60  
 Gly Leu Gly Ala Leu Arg Arg Glu Leu Ile Glu Ser Val Gly Phe Ala  
 65 70 75 80  
 Arg Ala Arg Gly Ile Met Leu Arg Thr Gly Tyr His Cys Gly Ala Lys  
 85 90 95

Asp	Ala	Ala	Leu	Leu	Lys	Glu	Arg	Phe	Ser	Asn	Ala	Asp	Pro	Leu	Ser	100	105	110
Leu	Phe	Ala	Ala	Gly	Pro	Asn	Leu	His	Ser	Leu	Glu	Gly	Ala	Val	Arg	115	120	125
Val	Glu	Pro	Ile	His	Phe	Asp	Phe	Asp	Met	Asp	Leu	Gly	Thr	Tyr	Tyr	130	135	140
Gly	Glu	Phe	Leu	Trp	His	His	Ser	Ser	Glu	Asp	Asp	Glu	His	Ile	Ala	145	150	155
His	Tyr	Gly	Ile	Gly	Thr	Glu	Pro	Ala	Cys	Trp	Thr	Gln	Thr	Gly	Tyr	165	170	175
Ala	Ile	Gly	Tyr	Thr	Ser	Ala	Leu	Val	Gly	Arg	Leu	Ile	Leu	Tyr	Arg	180	185	190
Glu	Val	Glu	Cys	Arg	Ser	Thr	Gly	Ser	Gln	Ile	Cys	Arg	Met	Ile	Gly	195	200	205
Lys	Pro	Ala	Glu	Glu	Trp	Glu	Asp	Ala	Glu	Glu	Asp	Leu	Ala	Ala	Leu	210	215	220
Ser	Ala	Thr	Ile	Cys	Arg	Gln	Pro	Ser	Thr	Pro	Gln	Arg	Arg	Arg	Thr	225	230	235
Gln	Gln	Gly	Gln	Arg	Asn	Thr	Pro	His	His	Ser	Ala	Ala	Asp	Ser	Ser	245	250	255
Thr	Ala	Ser	Glu	His	Asp	Met	Val	Gly	Ile	Ser	Ser	Ala	Phe	Asn	Ala	260	265	270
Ala	Cys	His	Met	Leu	Lys	Arg	Val	Ala	Pro	Thr	Glu	Ala	Thr	Val	Leu	275	280	285
Phe	Thr	Gly	Glu	Ser	Gly	Val	Gly	Lys	Glu	Met	Phe	Ala	Arg	Met	Leu	290	295	300
His	Arg	Ile	Ser	Pro	Arg	His	Asp	Gly	Pro	Phe	Val	Ala	Val	Asn	Cys	305	310	315
Ala	Arg	Ile	Pro	Glu	Thr	Leu	Met	Glu	Ser	Glu	Leu	Phe	Gly	Val	Glu	325	330	335
Arg	Gly	Ala	Phe	Thr	Gly	Ala	Thr	Gln	Ser	Arg	Ala	Gly	Arg	Phe	Glu	340	345	350
Arg	Ala	Ser	Gly	Gly	Thr	Leu	Phe	Leu	Asp	Glu	Ile	Gly	Thr	Leu	Ser	355	360	365
Leu	Val	Ala	Gln	Gly	Lys	Leu	Leu	Arg	Ala	Leu	Gln	Glu	Ser	Glu	Val	370	375	380
Glu	Arg	Val	Gly	Gly	Ser	Arg	Thr	Leu	Lys	Val	Asp	Val	Arg	Val	Val	385	390	395

Ala Ala Thr Asn Val Asp Leu Arg Ala Gly Val Gln Arg Gly Glu Phe  
                             405                            410                            415  
 Arg Glu Asp Leu Phe Phe Arg Leu Asn Val Tyr Pro Ile His Leu Pro  
                             420                            425                            430  
 Pro Leu Arg Glu Arg Lys Glu Asp Ile Pro Leu Leu Met Thr Tyr Phe  
                             435                            440                            445  
 Leu His Arg Phe Asn Gln Arg His Ser Arg Val Val Ser Gly Phe Thr  
                             450                            455                            460  
 Pro Arg Ala Ala Asn Ala Leu Leu Gly Tyr Asp Phe Pro Gly Asn Ile  
                             465                            470                            475                            480  
 Arg Glu Leu Gln Asn Leu Val Glu Arg Gly Val Ile Ser Ala Pro Glu  
                             485                            490                            495  
 Asp Gly Ala Ile Asp Val Ser His Leu Phe Thr Ser Gly Glu Arg Leu  
                             500                            505                            510  
 Thr Gln Pro Met Phe Ser Ile Gly Ala Ser Gly Ile Leu Ala Thr Ala  
                             515                            520                            525  
 Gln Asp Asn Gln Pro Gln Glu Thr Gly Ser Pro Ser Thr Ser Phe Ser  
                             530                            535                            540  
 Lys Pro Thr Ser Thr Ile Asp Ser Pro Leu Asp Ser Lys Asp Leu Ser  
                             545                            550                            555                            560  
 Ala Met Thr Leu Gln Glu Val Glu Asp Ala Met Ile Ser His Ala Leu  
                             565                            570                            575  
 Gly Gln Val Lys Gly Asn Val Ser Glu Ala Ala Arg Arg Leu Gly Leu  
                             580                            585                            590  
 Thr Arg Ala Gln Leu Ser Tyr Arg Ile Ser Arg Arg Pro Leu Asp Lys  
                             595                            600                            605

<210> 41

<211> 768

<212> DNA

<213> Pseudomonas sp.

<220>

<221> CDS

<222> (1)..(765)

<223> product = "Coniferylalcohol-Dehydrogenase" / gene  
                   = "cadh"

<400> 41

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 Met Gln Leu Thr Asn Lys Lys Ile Val Val Thr Gly Val Ser Ser Gly

1	5	10	15	
atc ggt gcc gaa act gcc cgc gtt ctg cgc tct cac ggc gcc aca gtg	96			
Ile Gly Ala Glu Thr Ala Arg Val Leu Arg Ser His Gly Ala Thr Val				
20	25	30		
att ggc gta gat cgc aac atg ccg agc ctg act ctg gat gct ttc gtt	144			
Ile Gly Val Asp Arg Asn Met Pro Ser Leu Thr Leu Asp Ala Phe Val				
35	40	45		
cag gct gac ctg agc cat cct gaa ggc atc gat aag gcc atc tct cag	192			
Gln Ala Asp Leu Ser His Pro Glu Gly Ile Asp Lys Ala Ile Ser Gln				
50	55	60		
ctg ccg gag aaa att gac gga ctc tgc aat atc gcc ggg gtg ccc ggc	240			
Leu Pro Glu Lys Ile Asp Gly Leu Cys Asn Ile Ala Gly Val Pro Gly				
65	70	75	80	
act gcc gat cct cag ctc gtc gca aac gtg aac tac ctg ggt cta aag	288			
Thr Ala Asp Pro Gln Leu Val Ala Asn Val Asn Tyr Leu Gly Leu Lys				
85	90	95		
tat ctg acc gag gca gtc ctg tcg cgc att caa ccc ggt ggt tcg att	336			
Tyr Leu Thr Glu Ala Val Leu Ser Arg Ile Gln Pro Gly Gly Ser Ile				
100	105	110		
gtc aac gtg tcc tct gtg ctt ggc gcc gag tgg ccg gcc cgc ctt cag	384			
Val Asn Val Ser Ser Val Leu Gly Ala Glu Trp Pro Ala Arg Leu Gln				
115	120	125		
ttg cat aag gag ctg ggg agt gtt gtt gga ttc tcc gaa ggc cag gca	432			
Leu His Lys Glu Leu Gly Ser Val Val Gly Phe Ser Glu Gly Gln Ala				
130	135	140		
tgg ctt aag cag aat cca gtg gcc ccc gaa ttc tgc tac cag tat ttc	480			
Trp Leu Lys Gln Asn Pro Val Ala Pro Glu Phe Cys Tyr Gln Tyr Phe				
145	150	155	160	
aaa gaa gca ctg atc gtt tgg tct caa gtt cag gcg cag gaa tgg ttc	528			
Lys Glu Ala Leu Ile Val Trp Ser Gln Val Gln Ala Gln Glu Trp Phe				
165	170	175		
atg agg acg tct gta cgc atg aac tgc atc gcc ccc ggc cct gta ttc	576			
Met Arg Thr Ser Val Arg Met Asn Cys Ile Ala Pro Gly Pro Val Phe				
180	185	190		
act ccc att ctc aat gag ttc gtc acc atg ctg ggt caa gag cgg act	624			
Thr Pro Ile Leu Asn Glu Phe Val Thr Met Leu Gly Gln Glu Arg Thr				
195	200	205		
cag gcg gac gct cat cgt att aag cgc cca gca tat gcc gat gaa gtg	672			
Gln Ala Asp Ala His Arg Ile Lys Arg Pro Ala Tyr Ala Asp Glu Val				
210	215	220		
gcc gcg gtg att gca ttc atg tgt gct gag gag tca cgt tgg atc aac	720			
Ala Ala Val Ile Ala Phe Met Cys Ala Glu Glu Ser Arg Trp Ile Asn				
225	230	235	240	

ggc ata aat att cca gtg gac gga ggt ttg gca tcg acc tac gtg taa 768  
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 <212> PRT  
 <213> Pseudomonas sp.

<400> 42  
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           20                  25                  30  
 Ile Gly Val Asp Arg Asn Met Pro Ser Leu Thr Leu Asp Ala Phe Val  
           35                  40                  45  
 Gln Ala Asp Leu Ser His Pro Glu Gly Ile Asp Lys Ala Ile Ser Gln  
   50                  55                  60  
 Leu Pro Glu Lys Ile Asp Gly Leu Cys Asn Ile Ala Gly Val Pro Gly  
   65                  70                  75                  80  
 Thr Ala Asp Pro Gln Leu Val Ala Asn Val Asn Tyr Leu Gly Leu Lys  
           85                  90                  95  
 Tyr Leu Thr Glu Ala Val Leu Ser Arg Ile Gln Pro Gly Gly Ser Ile  
          100                 105                 110  
 Val Asn Val Ser Ser Val Leu Gly Ala Glu Trp Pro Ala Arg Leu Gln  
          115                 120                 125  
 Leu His Lys Glu Leu Gly Ser Val Val Gly Phe Ser Glu Gly Gln Ala  
          130                 135                 140  
 Trp Leu Lys Gln Asn Pro Val Ala Pro Glu Phe Cys Tyr Gln Tyr Phe  
  145                 150                 155                 160  
 Lys Glu Ala Leu Ile Val Trp Ser Gln Val Gln Ala Gln Glu Trp Phe  
          165                 170                 175  
 Met Arg Thr Ser Val Arg Met Asn Cys Ile Ala Pro Gly Pro Val Phe  
          180                 185                 190  
 Thr Pro Ile Leu Asn Glu Phe Val Thr Met Leu Gly Gln Glu Arg Thr  
          195                 200                 205  
 Gln Ala Asp Ala His Arg Ile Lys Arg Pro Ala Tyr Ala Asp Glu Val  
          210                 215                 220  
 Ala Ala Val Ile Ala Phe Met Cys Ala Glu Glu Ser Arg Trp Ile Asn  
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Gly Ile Asn Ile Pro Val Asp Gly Gly Leu Ala Ser Thr Tyr Val  
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Ser Ala Leu Xaa  
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